

STIC Database Tracking Number: 145765

TO: Terry McKelvey

Location: REM-2A75&2C70

Art Unit: 1636

Saturday, March 05, 2005

Case Serial Number: 10/006116

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner McKelvey,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527





Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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	vasotocin - Pacifi			161	4. 4 U U	5 G	1451	
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	hypothetical prote			560		ง ผ	1419	
	hypothetical prote			532		2	1418	
	probable beta-lact			498	4.5	2	1417	

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ENTS ENTS Tul-1996 #text_ch a, Y.; Suzuki, J. changes of a nov pMID:7623137 EMBL/DDBJ EMBL/DDBJ	IRMIMRN : IKKTMDN			Simi 1;	mouse lis musculus lis musculus lis musculus lis f659 15659 1, 5088-5 15, 5088-5 15, 5088-7 15, 508		444444444
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in precial preciary preciars preciary preciary in glyci larger protes of tor-6. Proteinal elon larger protease general elon serine protease general elon larger protes of tor-6. PUTAA 61				622.5; DB 2; Length 260; NO. 3.2e-43; matches 93; Indels 5; Gaps 3	Jul-1996 #text_change 09-Jul-2004 a, Y.; Suzuki, J.; Tanaka, T.; Ito, changes of a novel limbic-serine pr PMID:7623137 EMBL/DDBJ	IGNMENTS	hypothetical personal interest in hemagglutinin hydrogenase-2 epithelin/grar hypothetical protein kinase hypothetical protein protein protein protein en from the following in the following protein death receptor the following protein from the following protein pr

RESULT 2
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trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N;Alternate names: trypsinogen II
C;Species: Gallus gallus (chicken)
C;Apecies: Gallus gallus (chicken)
C;Accession: S5066; S72347
C;Accession: S5066; S72347
E,Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A;Title: Isolation and characterization of the chicken trypsinogen gene family.
A;Reference number: S5065; MUID:95251611; PMID:7733885
A;Residues: 1-248 <WAN1>

Indels

12;

Gaps

59

proteinase; zymogen

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A;Residues: 1-248 <WAN1>
A;Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; EMBL:U15156; NII
A;Experimental source: clone 1-938
A;Accession: $72345
A;Molecule type: DNA
A;Residues: 1-248 <WAN2>
A;Accession: $5065
A;Accession: $55065
A;Accession: $55065
A;Molecule type: mRNA
A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN3>
A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN3>
A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN3>
A;Cross-references: EMBL:U15155; NID:g603902; PIDN:AAA79912.1; PID:gA;Accession: $72346
               submitted to the EMBL Data Library, A;Reference number: $71155
                                                                                 A;Molecule type: DNA
A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248
A;Cross-references: GB:U15155; NID:g603902; PIDN:AAA79912.1;
A;Experimental source: clone PI
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N;Alternate names: trypsinogen I
C;Species: Gallus gallus (chicken)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: S55067; S72345; S55065; S72346; S71155
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Biochem. J. 307, 471-479, 1995
A; Title: Isolation and characterization of A; Reference number: S55065; MUID:95251611;
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A; Residues: 1-248 < WA
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A;Bxperimental source: clone 2-P29
C;Superfamily: trypsin; homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zyme
F;1-16/Domain: stgnal sequence #status predicted <STG>
F;17-25/Domain: strypsin II #status predicted <APT>
F;26-248/Product: trypsin II #status predicted <APT>
F;26-241/Domain: trypsin homology <TRY>
F;26-241/Domain: trypsin homology <TRY>
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A;Experimental source: clone 2-p29
A;Accession: S72347
A;Molecule type: DNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWIR 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTSSVQPLPLPNDCATAGTECHVSGWGITNHERNPFPDLLQCLNLSIVSHATCHGVYPGR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAHCYKSRIQVRLGEYNIDVQEDSEVVRSSSVIIRHPKY--SSITLNNDIMLIKLASAVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLIRLRLPVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFLTLSCLGAAVAFPGGADDDKIVGGYTCPEHSVPYQVSLNSGYHF-CGGSLINSQWVLS
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47.5%;
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Pred. No. 6e
                                          September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIPROT: Q90628; EMBL: U15156; NID: g603904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g6039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the chicken trypsinogen PMID:7733885
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78;
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                                                                                                         PID:g603903
                                                                                                                                      <WAN4>
                                                                                                                                                                                                                                  PID:g603903
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                                                                                    A;Note: at position 20, Ile and Val occur alternatively (;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; pancreas; polymorphism; protein digestion; F;1-231/Product: trypsingen #status experimental <ZYM>F;1-8/Domain: activation peptide #status experimental <APT>F;9-231/Product: trypsin #status experimental <APT>F;9-231/Product: trypsin #status experimental <APT>F;9-231/Product: trypsin #status experimental <APT>F;9-24/Domain: trypsin homology <TRY>F;15-145,33-49,117-218,124-191,156-170,181-205/Disulfide bonds: #sf;48,92,185/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A90368; MUID:73258692; PMID:4738933 A;Accession: A90368
                                                                    F;60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu)
                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 9-231 < HER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Hermodson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A. Biochemistry 12, 3146-3153, 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
N;Contains: trypsinogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change
C;Accession: A90641; A90388; A00947
R;Charles, M.; Rovery, M.; Guidoni, A.; Desnuelle, P.
Biochim. Biophys. Acta 69, 115-129, 1963
A;Tittle: Su le trypsinogene et la trypsine de porc.
A;Reference number: A90641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-10 < CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A90641
A; Accession: A90641
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C;Superfamily: trypsin; trypsin homology
C;Kuywords: hydrolase; pancreas; protein digestion; serine
F;1-15/Domain: signal sequence #status predicted <APT>
F;16-25/Domain: activation peptide #status predicted <APT>
F;26-248/Product: trypsin I #status predicted <MAT>
F;26-241/Domain: trypsin homology <TRY>
F;26-241/Domain: trypsin homology <TRY>
F;26-241/Domain: trypsin homology <TRY>
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A;Molecule type: mRNA
A;Residues: 1-102,'A',104-248 <WANS>
A;Cross-references: EMBL;U15156; NID:g603904; PIDN:AAA79913.1; PID:g603905
     Best Local
                               Query Match
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 PVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVY
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  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVLVAFLGVAVAFPISDEDDDKIVGGYSCARSAAPYQVSLNSGYHF-CGGSLISSQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSIFLLLCVLG-----LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRW 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATLNSYVNTVPLPTSCVTAGTTCLISGWGNTLSSGSLYPDVLQCLNAPVLSSSQCSSAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGRITSNMICIGYLNGGKDSCQGDSGGPVVCNGQLQGFVSWG-IG-CAQKGYPGVYTKVC
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     40.8%;
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45.5%; Pred. No. 9.
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     Score
Pred.
     No.
2.7e-38;
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                                                                 Glu) #status predicted
                  Length 231;
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trypsin

by sequenator

analys

09-Jul-2004

235

235

177 176

#status predicted

serine

proteinase;

zymo

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C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; protein digestion; serine proteinase
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-20/Domain: activation peptide #status predicted <APT>
F;21-236/Domain: trypsin homology <TRY>
F;26-243/Product: trypsin I #status predicted wATS
F;27-157,45-61,129-230,136-203,168-182/Disulfide bonds: #status predicted
F;60,104,197/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog (;Species: Xenopus laevis (African clawed frog) c;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004 C;Accession: A35871; S12117 R;Shi, Y.B.; Brown, D.D. Genes Dev. 4, 1107-1113, 1990 Genes Dev. 4, 1107-1113, 1990 A;Title: Developmental and thyroid hormone-dependent regulation of pancreat: A;Reference number: A35871; MUID:91007255; PMID:2210372 A;Accession: A35871 A;Status: preliminary A;Status: preliminary
serine proteinase SCCE precursor -
N;Alternate names: stratum corneum
C;Species: Homo sapiens (man)
                                                             RESULT
A53968
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A;Residues: 1-243 <SHI>
A;Cross-references: UNIPROT:P19799; EMBL:X53458; NID:g65162;
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Matches 113; Conserv
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                                                                                                                                                                                                                                             NMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWI 241
                                                                                                                                                                                                                                                                                                                                                 SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LISGWGNTKSSGSSYPSLLQCLKAPVLSDSSCKSSYPGQITGNMICVGFLEGGKDSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC
                                                                                                                                                                                    RMIMRNN 248
                                                                                                                                                                                                                                                                                                           AVNTVPLPSGCSAAGTSCLISGWGNTLSNGSNYPDLLQCLNAPILTNAQCNSAYPGEITA
                                                                                                                                                                                                                                                                                                                                                                                            CYKASIQVRLGEHNIALSEGTEQFISSSKVIRHSGY--NSYTLDNDIMLIKLSSPASLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLLLCVL-LGAAAAFDDDKIIGGATCAKSSVPYIVSLNSGYHF-CGGSLITNQWVVSAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLLLCVLGLSQAAT---PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGNEQFINAAKIITHPNFNG--NTLDNDIMLIKLSSPATLNSRVATVSLPRSCAAAGTEC
                                                                                                                                              ONTIAAN
                                                                                                                                                                                                                            NMI CVGYMEGGKDS CQGDSGGPVVCNGQLQGVVSWGY - -GCAMRNYPGVYTKVCNYNAWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGPVVCNGQLQGIVSWGY--GCAQKNKPGVYTKVCNYVNWIQQTIAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIVGGYTCAANSIPYQVSLNSGSHF-CGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.4%; Score 555; DB 2; 45.7%; Pred. No. 8.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Mismatches
                                          human
                     chymotryptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                       enzyme
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A;Molecule type: mRNA
A;Residues: 1-246 <STE>
A;Residues: 1-246 <STE>
A;Cross-references: UNIDROT:p07146; GB:X04574; NID:g54918; PIDN:CAA28243.1; PID:g54919
A;Cross-references: UNIDROT:p07146; GB:X04574; NID:g54918; PIDN:CAA28243.1; PID:g54919
C;Superfamily: trypsin; trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-246/Product: trypsin #status predicted <MAT>
F;24-219/Domain: trypsin homology <TRY>
F;24-219/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trypsin (EC 3.4.21.4) precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004 C;Accession: B2528 R;Stevenson, B.J.; Hagenbuschle, O.; Wellauer, P.K. Nucleic Acids Res. 14, 8307-8330, 1978 Nucleic Nucleic Acids Res. 14, 8307-8330, 1978 Nucleic Nuclei
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C;Superfamily: trypsin; trypsin ho
F;30-245/Domain: trypsin homology
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A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
C;Genetics:
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Best Local
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Accession: A53968
                                                                                                                                               Matches
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MSALLILALVGAAVAFPVDDDDKIVGGYTCRESSVPYQVSLNAGYHF-CGGSLINDQWVV
                                                                     LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
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Pred. No. 9.2e-38;
                                                                                                                                           Score 553; DB 2;
Pred. No. 1.3e-37;
5; Mismatches 81
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A;Note: the sequence agrees with that shown

A;Note: the sequence agrees with that shown

R;Bode, W.; Schwager, P.

J. Mol. Biol. 98, 693-717, 1975

A;Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution

A;Reference number: A92954; MUID:76072097; PMID:512

A;Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a termi

C;Comment: Autocatalytic cleavage and also occur after Arg-105.

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F;1-229/Product: trypsin open #status experimental <ZYM>

F;1-29/Product: trypsin homology <TRY>

F;7-131,132-229/Product: alpha-trypsin #status experimental <APT>

F;7-31,132-229/Product: alpha-trypsin #status experimental <APT>

F;7-314,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: #status experimental

F;46,90,183/Active site: His, Asp, Ser #status experimental

F;58,60,63,68/Binding site: Calcium (Glu, Asn, Val, Glu) #status experimental

F;131-132/Cleavage site: Lys-Ser (autolytic) #status experimental
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence revision 28-Feb-1986 #text_change 18-Jul-1997
C;Accession: A90164; A00946; S08774
C;Accession: A90164; A00946; S08774
R;Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.
Biochem: Biophys. Res. Commun. 24, 346-352, 1966
A;Title: Covalent structure of bovine trypsinogen. The position of the rema
A;Reference number: A90164; MUID:67168848; PMID:5967094
                                                                                                                                                                 S
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R; Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh,
Biochemistry 14, 1358-1366, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Amino acid sequence of dogfish trypsin. A; Reference number: A00950; MUID: 75146445; PMID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A93755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hartley, B.S.
Philos. Trans. R. Soc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-57,'Q',59-67,'Q',69-150,'N',152-176,'N',178-229
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                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                      106;
           65
                                            81 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQFLFLPNDCATAGTEC 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           annotation; revisions
                                                                                                                                                   KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
EGNEOFISASKSIVHPSY--NSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTOC
                                                                                                 KIVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLNARVASVPLPSSCAPAGTQCLISGWGNTLSNGVNN--PDLLQCVDAPVLPQADCEASY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGDITNNMICVGFLEGGKDSCQGDSGGFVVCNGELQGIVSWGY--GCAQPDAPGVYTKVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVTSSVQPLPLPNDCATAGTECHVSGWG---ITNHPRNPFPDLLQCLNLSIVSHATCHGVY
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                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                              40.2%; Score 552; DB 1;
46.3%; Pred. No. 1.4e-37;
tive 40; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
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                                                                                                                                                                                                                                                                Length 229
                                                                                                                                                                                                                 Indels
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122
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C; Superfa
C; Keyword
F; 24-239/
F; 63, 107,
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A;Residues: 1-247 cHUE>
A;Residues: 1-247 cHUE>
A;Cross-references: UNIPROT:Q29463; EMBL:X54703; NID:g829; PIDN:CAA38513.1; PID:g830 C;Superfamily: trypsin; trypsin homology C;Superfamily: trypsin; trypsin digestion; serine proteinase
C;Keywords: hydrolase; protein digestion; serine proteinase
E;24-239/Domain: trypsin homology cTRY>
C;Keywords: hydrolase; protein digestion; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,40 nuerou, I.; Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A. Eur. J. Biochem. 193, 767-773, 1990
A,Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic anionic A;Reference number: S13813; MUID:91065383; PMID:1701147
A;Accession: S13813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypsin (EC 3.4.21.4) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Dec-193 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Datession: S13813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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                                                                                                                                              183
                                                                                                                                                                                                  122
                                                                                                 182
                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                                            64 CYQYHIQVRLGEYNIDVLEGGEQFIDASKIIRHPKY--SSWTLDNDILLIKLSTPAVINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                  RMIMRNN
                                                                                                                                 NMVCAGGVP-GQDACQGDSGGBLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWI 241
                                                                                                                                                                                        RVSTLLLPSACASAGTECLISGWGNTLSSGVNYPDLLQCLVAPLLSHADCEASYPGQITN
                                                                                                                                                                                                                               SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS 182
QETIAAN
                                                                                         NMICAGFLEGGKDSCQGDSGGPVACNGQLQGIVSWGY--GCAQKGKPGVYTKVCNYVDWI
                                                                                                                                                                                                                                                                                                                                           CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS
                                                                                                                                                                                                                                                                                                                                                                                              LILAFVGAAVAFPSDDDDKIVGGYTCAENSVPYQVSLNAGYHF-CGGSLINDQWVVSAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGPVVCSGKLQGIVSWGS--GCAQKNKPGVYTKVCNYVSWIKQTIASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                            248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 550; DB 2; 45.7%; Pred. No. 2.3e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                         239
                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                63
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trypsin (EC 3.4.21.4) precursor, anionic - N;Alternate names: cationic trypsinogen C;Species: Canis lupus familiaris (dog) C;Date: 30-Sep_1987 #sequence_revision 30dog

30-Sep-1987 #text_change 09-Jul-2004

C;Accession: A26273
R;Pinsky, S.D.; LaFozge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation:
A;Reference number: A26273; MUID:86284628; PMID:3841794
A;Accession: A26273 full-length mRNA

A;Molecule type: mRNA
A,Residues: 1-247 <PIN>
A,Residues: 1-247 <PIN>
A,Residues: 1-247 <PIN>
A;Cross-references: UNIPROT:P06872; GB:M11589; NID:g164094; PIDN:AAA30899.1; PID:g164095
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

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trypsin (EC 3.4.21.4) precursor, cationic - dog
N,Alternate names: cationic trypsinogen
C;Species: Canis lupus familiaris (dog)
C;Species: Ocanis lupus familiaris (dog)
C;Species: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: B26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque
A;Reference number: A26273; MUID:86284628; PMID:3841794
A;Accession: B26273
A;Molecule type: mRNA
A;Residues: 1-246 <PINN
A;Cross-references: UNIPROT:P06871; GB:M11590; NID:g164096; PIDN:AAA30900.1; PID:g164097
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;15-15/Domain: activation peptide #scatus predicted <APT>
F;24-23/Domain: activation peptide #scatus predicted <APT>
F;24-23/Jomain: trypsin homology <TRY>
F;30-160,48-64,132-23,139-206,717-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
TRDGC
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F;24-247/Product: trypsin, anionic #status predicted <ENZ>
F;24-239/Domain: trypsin homology <TRY>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted F;63,107,200/Active site: His, Asp, Ser #status predicted F;63,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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Best Local S
Matches 111
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                                          119 RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRIT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLCVLGLSQAATP----KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
                                                                                                                                                                                     MKTFIFLALLGATVAFFIDDDDKIVGGYTCSRNSVFYQVSLNSGYHF-CGGSLINSQWVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRMIMRNN
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TLNSRVSAIALPKSCPAAGTQCLISGWGNTQSIGQNYPDVLQCLKAPILSDSVCRNAYPG
                                                                                                                                      TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV 118
                                                                                                                                                                                                                               LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
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45.6%;
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                                                                                                                                                                                                                                                                              Score 545; DB 1;
Pred. No. 5.8e-37;
43; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 546; DB 1; Length 247; Pred. No. 4.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                              Length 246;
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A;Molecule type: mRNA
A;Residues: 1-247 <FLE>
A;Cross-references: UNIPROT: P08426; GB:M16624; NID:g206498; PIDN:AAA41985.1;
A;Cross-references: UNIPROT: P08426; GB:M16624; NID:g206498; PIDN:AAA41985.1;
C;Superfamily: trypsin; trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;25-240/Domain: trypsin homology <TRY>
F;35-240/Domain: trypsin homology <TRY>
F;31-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;67,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trypsin (EC 3.4.21.4) precursor, cationic - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #te C;Accession: A27547 R;Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, Biochemistry 26, 3081-3086, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Isolation and characterization of a cDNA encoding A,Reference number: A27547; MUID:87271609; PMID:3607011 A,Accession: A27547
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                                                                                                                                                                                                                                                                                        LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLP 117
                                                                                                                                                                                                                                                                                                                                                                         LSIFLLLCVLGLSQAA----TPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV
                                                                               GKITSNMFCLGFLEGGKDSCQGDSGGPVVCNGQLQGVVSWGY--GCAQKGKPGVYTKVCN 235
                                                                                                         GRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICK 236
                                                                                                                                                                                                      VRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYP 177
                                                                                                                                                                                                                                                                                                                                   MKALIFLAFLGAAVALPLDDDDDKIVGGYTCQKNSLPYQVSLNAGYHF-CGGSLINSQWV 59
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                                      YVDWIRMIMRNN
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                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 544.5; DB 2;
Pred. No. 6.3e-37;
3; Mismatches 89;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-246 <CRA>
A;Residues: 1-246 <CRA>
A;Cross-references: UNIPROT:P00762; GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A;Cross-references: UNIPROT:P00762; GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 170
R;MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
                                                                                                                                                                                                                                                                                                                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 09-Jul-2004
C;Accession: B22657; A00948
R;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, J. Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
A;Accession: B22657
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trypsin (EC 3.4.21.4) I precursor - rat N;Alternate names: trypsinogen I C;Species: Rattus norvegicus (Norway rat C;Date: 17-Dec-1928 #sequence_revision I C;Accession: B22657; A00948

Rutter,

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TRRT1 RESULT 13

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C;Superfamily: trypsin, trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-7/Domain: signal sequence (fragment) #status predicted <SIG>F;8-15/Domain: activation peptide #status predicted <APT>F;16-238/Product: trypsin III #status predicted <AMT>F;16-238/Domain: trypsin homology <TRY>F;16-231/Domain: trypsin homology <TRY>F;16-231/Domain: trypsin homology <TRY>F;15-231/Domain: trypsin homology <TRY>F;22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status F;55,99,192/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P35033; EMBL:X70074; NID:g64387; PIDN:CAA49679.1; C;Superfamily: trypsin; trypsin homology
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A; Residues: 1-238 < MAL>
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A;Introns: 14/1; 67/2; 152/1; 197/3
A;Introns: 14/1; 67/2; 152/1; 197/3
C;Superfamily: trypsin; trypsin homology
C;Reywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen C;Reywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen F;115/Domain: activation peptide #status predicted <APT>
F;16-23/Domain: activation peptide #status predicted <APT>
F;24-246/Product: trypsin I #status predicted <ENZ>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted F;33,107,200/Active site: His, Asp, Ser #status predicted predicted F;37,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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;Residues: 1-246 <MAC>
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Accession: A00948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
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Similarity 44.5%; Pred. No. 8.4e-37;
10; Conservative 47; Mismatches 70
KIVGGYECRKNSASYQASIQSGYHF-CGGSLISSTWVVSAAHCYKSRIQVRLGEHNIAVN 73
                                                  KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
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                                                                                                                                        39.3%; Score 540;
47.2%; Pred. No. 1
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                                                                                                                            No.
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/. 1.4e-36;
78;
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S05494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trypsin (RC 3.4.21.4) IV precursor - rat
N;Alternate names: 23K protein; trypsinogen IV precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
C;Accession: S05494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-247 < LUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Juetcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F. Nucleic Acids Res. 17, 6736, 1989
A;Tille: A fourth trypsinogen (P23) in the rat pancreas induced by A;Reference number: S05494; MUID:89386010; PMID:2780302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S05494
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                                           VDWIRMIMRNN 248
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                                                                                                                                                                                                                                                                                 SAAHCYKRKLOVRLGEHNIHVLEGGEOFIDAEKIIRHPEY--NKDTLDNDIMLIKLKSPA 118
                                                                                                                                                                                                                                                                                                                                                                            MKISIFFAFLGAAVALPVNDDDKIVGGYTCPKHLVPYQVSLHDGISHQCGGSLISDQWVL
                                                                                        QITSNMFCLGFLEGGKDSCDGDSGGPVVCNGEIQGIVSWGSV--CAMRGKPGVYTKVCNY 236
                                                                                                                                                                                   VLNSQVSTVSLPRSCASTDAQCLVSGWGNTVSIGGKYPALLQCLEAPVLSASSCKKSYPG
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TANDARD; PRT; 248 AA. 40, Created) 40, Last sequence update) 41, Last annotation update) ecursor (EC 3.4.21) (Kallikrein /PRO1303) man). Chordata; Craniata; Vertebratia; Primates; Catarrhini; Hominid A. (ISOFORM 1). PubMed=10652563; LY. Diamandis E.P.; of novel human kallikrein-like ge 19:2843-2852(1999). A. (ISOFORMS 1 AND 2). klara A., Scorilas A., Diamandis alternatively spliced forms of th "; pp) to the EMBL/GenBank/DDBJ dat A. (ISOFORM 1). POI=10.1016/S0378-1119(00)00382-881th R., Argonza-Barrett R., Lei B., Wang K.; PDOI=10.1016/S0378-1119(00)00382-881th R., Argonza-Barrett R., Lei B., Wang K.; (2000) DOI-10.1016/S0378-1119(00)00382-881th R., Argonza-Barrett R., Lei B., Wang K.; Smith R., Argonza-Barrett R., Bald Chui C., Crowley C., Currell B. Chui C., Crowley C., Currell B. J., Grimaldi C., Gu O., Hass P.E S., Klimowski L., Jin Y., Johnson Mark M., Robbie E., Sanchez C. mmons L., Singh J., Smith V., Stinabe C., Wieand D., Woods K., Xie an J., Zhang M., Zhang Z., Goddar Y.A.; Chang M., Zhang Z., Goddar Y.A.; Olsen A.S., Terry A., Selon L.A., Olsen A.S., Terry A., Selon L.A., Olsen A.S., Couronn T.M., Ashworth L., Bajorek E., Bl Trano A.V., Caoile C., Chan Y.M., peland A., Dalin E., Dehal P., De	0 374 2 Q80YD5 0 392 2 Q9VMZ3 0 401 2 Q6LHI7 0 260 2 Q9U4I4 0 291 2 Q6YIY9 0 243 2 Q7M4I3 0 278 2 Q7W6J5 0 350 2 Q9VCJ9 0 360 2 Q9WIX6
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GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; F:serine-type endopeptidase activity; NAS.

GO; GO:0004252; F:serine-type endopeptidase activity; NAS.

GO; GO:0004508; P:proteolysis and peptidolysis; NAS.

InterPro; IPR009003; Pept Ser Cys.

R InterPro; IPR001254; Peptidase_S1.

R Pfam; PF0001314; Peptidase_S1A.

R Pfam; PF00089; Trypsin; 1.

R PRINTS; PR00022; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

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EMBL; AV358524; AAQ88888.1; ...
EMBL; AC011473; AAQ88888.1; ...
HSSP; P00760; 1EZX.
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MIN; 605539; ...
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  Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDN prepare full-length cDNA libraries for rapid discovery of Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/65; TISSUE=Tongue;
MEDLINE=20499374; PubMed=11042159;
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cMeth. Enzymol. 303:19-44(1999).
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Nature 420:563-573(2002).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310008B01 product:similar to KALLIKREIN 12 (EC
3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Klk12
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10; PubMed=11217851; DOI=10.1038/35055500;
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Sciurognathi; Muridae; Murinae;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                      h Group
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Best Local
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GG; GO:0004263; F:chymotrypsin activity; IEA.
GG; GO:0004295; F:trypsin activity; IEA.
InterPro; IPR001325; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; PF000089; Trypsin; 1.
PRINTS; PR000125; Trypsin; 1.
RPNOSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN JER; UNKNOWN 1.
PROSITE; PS00134; TRYPSIN JER; 1.
PROSITE; PS00135; TRYPSIN JER; 1.
PROSITE; PS00134; TRYPSIN JER; 1.
PROSITE; PS00135; TRYPSIN JER; 1.
PROSITE; PS00134; TRYPSIN JER; 1.
PROSITE; PS00135; TRYPSIN JER; 1.
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PROSITE; PS00134; TRYPSIN JER; 1.
PROSITE; PS00135; TRYPSIN JER; 1.
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STRAIN-C57BL/63; TISSUE=Tongue;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Tongue;

MEDLINB=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; 1
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                                                                                                                                                                                         ATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPGQ 193
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                                                                                                                                                                                                                                                                                                                                               EHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLFVRVTSSVQPLPLPNDC
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DACQGDSGGPLVCGGVLQGLVSWGSVGPCGQKGIPGVYTKVCKYTDWIRIVIRNN
                                                                       DACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN
                                                                                                                                                      VTTGAMCHVSGWGTTNKPWDPFPDRLQCLNLSTVSNETCRAVFPGRVTENMLCAGGEAGK
                                                                                                                                                                                                                                                                                                        EHSLTKLDWTEQLRHTTFSITHPSYQGAYQNHEHDLRLLRLNRPIHLTRAVRPVALPSSC
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RESULT 3 KLK8_HUMAN

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SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=22897296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Clark H.F., Gurney A.C., Crowley C., Currell B., Deuel B., Dowd P.

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.

Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimwoski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagits A.,

Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., VanBura D.,

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

Godowski P., Gray A.;

The secretal market in discovery initiative (SDNI) a large-scale
                                    SEQUENCE
Lamerdin
                                                                                       "The secreted protein discovery effort to identify novel human s bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein protease TADG-14) (Tumor-associated differentially protein) (UNQ283/PRO322).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLK8_HUMAN STANDARD; PRT; 260 AA.
060259; 09HCB3; Q9UIL9; Q9UQ47;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21,-) (NP) (Kallikrein 8) (Ovasin) (Serine
                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11054574;
Gan L., Lee I., S
Moss P., Paeper E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K., "Molecular cloning and characterization of a novel serine proteous in a potential molecular marker for ovarian carcinomas."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Brien T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE=99413504; PubMed=10485494;
Underwood L.J., Tanimoto H., Wang Y., Shigemasa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   generated by alternative human adult brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitsui S., Tsuruoka N., Yamashiro "A novel form of human neuropsin, generated by alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Hippocampus;
MEDLINE=98372070; E
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=KLK8; Synonyms=NRPN, PRSS19,
Homo sapiens (Human)
   Burkhart-Schultz
Phan H., Velasco
                                                                                                                                                                                                                                                                                                                                                                          Gene
                                                                                                                                                                                                                                                                                                                                                                                         "Sequencing and expression analysis of the serine protease cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning of tumor-associated differentially expressed "Cloning of tumor-associated by ovarian carcinoma.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99203457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98372070; PubMed=9714609; DOI=10.1016/S0378-1119(98)00232-7;
Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
"Sequence analysis and expression of human neuropsin cDNA and gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Res. 59:4435-4439(1999).
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OF 1-164 FROM N.A. (ISOFORM 1).
J.E., MCCready P.M., Skowronski E., Visw
-Schultz K., Gordon L., Dias J., Ramirez
Velasco N., Do L., Regala W., Terry A.,
                                                                                                                                                                                                                                                                                                                                                                                                                        1054574; DOI=10.1016/S0378-1119(00)00382-6;
Lee I., Smith R., Argonza-Barrett R., Lei H.,
Paeper B., Wang K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A. (ISOFORM 1).
Gelinas R., Gown A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A. (ISOFORM 1)
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Catarrhini; Hominidae;
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                                                                                                                          initiative (SPDI), a large secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K., Nakazato H., Yamaguchi N.; a brain-related serine protease, and is expressed preferentially
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Viswanathan V.,
direz M., Stilwagen
A., Brower A., Ga:
                                                                                                                                              a large-scale
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                                                                                                                                                                                                                                                           00 MIM,
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PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                       Genew; HGNC: 6369;
                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as green
modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A Olsen A.S., Carrano A.V., "Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Suggested to be involved in kindling epileptogene hippocampal plasticity.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
-!- SUBCELULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId-060259-2; Sequence=VSP 005401; TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in pancreas while isoform 2 is expressed in adult brain and hippocampus. Both forms are also found in fetal brain and placenta. Not detected in kidney, spleen, liver and lung. SIMILARITY: Belongs to the peptidase SI family. Kallikrein
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   IsoId=060259-1;
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PS00134; TRYPSIN HIS; 1.
PS00135; TRYPSIN SER; 1.
                                                                                                                                                           splicing;
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                                                                                                                                                           Glycoprotein;
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Potential.
By similarity.
Neuropsin.
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Charge relay sy
Charge relay sy
By similarity.
N-linked (Glona,
A -> AACGSLDLLT)
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                                                                                                                                                           Hydrolase;
            (GlcNAc.
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RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RS Klausher R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farner A.A., Schanici P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,
Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Nanca S.J., Marra M.A.,
"Genera E.D., Schnerch A., Schein J.E.,
"Genera E.D., Schnerch A., Sche
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Best Local S
Matches 123
Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; BC040887; AAH40887.1; -.
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Mammalia; Eutheria;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Kallikrein 8, isoform 1
                                                                                                                         2
                                                                                                                                                                               "Generation and initial analysis
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TISSUE=Brain;
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Pred. No. 1.3e-42;
"" matches 93;
                                                                                                                                        99:16899-16903 (2002)
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EF439E5B8C83E660 CRC64;
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                                                                                                                                                                           full-length
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R GO; GO:00004263; F:chymotrypsin activity; IEA.
R GO; GO:00004295; F:trypsin activity; IEA.
R GO; GO:0004295; F:trypsin activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEI
InterPro; IPR001514; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
JR InterPro; IPR001314; Peptidase S1A.
JR InterPro; IPR001314; Peptidase S1A.
JR Pfam; PF00089; Trypsin; 1.
JR Pfam; PF00089; Trypsin; 1.
JR PROSITS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS50240; TRYPSIN DOM; 1.
DR PROSITE; PS50240; TRYPSIN HIS; UNKNOWN 1.
DR PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
DR PROSITE; PS00134; TRYPSIN SER; 1.
KW Hydrolase; Protease; Serine protease.
Hydrolase; Protease; Serine protease.
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Matches 123
                                                                                                                                                                                                                                MEDLINE-95348817; PubMed-7623137; Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki Chen Z.-L., Yoshida S., Kato K., Momota Y., Shiosaka Ito J., Nishino H., Aimoto S., Klyama H., Shiosaka "Expression and activity-dependent changes of a nov protease gene in the hippocampus."; O. Neurosci. 15:5088-5097(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21-) (NP) (Kallikrein Name=Kik8; Synonyms=Nrpn, Prss19;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=BALB/c; TISSUE=Hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRPN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
  STRAIN=Czech II;
                        SEQUENCE FROM
                                                                             Submitted
                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia;
                                                                                                                                                           Yoshida S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDVMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS-DPCGRSDKPGVYTNICRYLDW
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                                                                             (SEP-1999)
                                                                                                                                                        DM N.A.
Hirata A.,
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                                                                                                                               assignment
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TISSUE-Mammary gland
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28090 MW; EF5934EB96295660 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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50.2%; Pred. No. 2.2e
tive 24; Mismatches
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t of mo
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                                                                                                                         Shiosaka S.;
neuropsin gene,
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ches 93;
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                                                                                                                                                                                                                                                                                          limbic-serine
                                                                                                                                                                                                                                                                                                                                            Tanaka
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                                                                                                                                  chromosome
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MEROPS; S01.244; -. MGD; MGI:892018; Klk8

IPR009003;

Pept_Ser_Cys

1NPM; X-ray; A/B=33-256

I56559;

I56559

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Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Rabin G.M., Hong L.,
A Hopkins R.F., John M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Hopkins R.F., John M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Hopkins R.F., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bonffard G.G.,
A Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
A Hutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Tennamics C.M., Schein J.E., Jones S.J.M., Marra M.A.,
Tennamics C.M., Schein J.B., Jones S.J.M., Marra M.A.,
Tennamics C.M., Marra M.A.,
Tennamics C.M., Marra M.A.,
Tennamics C.M., Marra M.A.,
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Hippocampus;
MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
... Kato K., Matsumoto K., Yoshida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shiosaka S., Hakoshima T.; "Crystal structure of neuropsin, a hippocampal protease involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Sh "Characterization of recombinant and brain neuropsin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/c; TISSUE=Brain; STRAIN=BALB/c; TISSUE=Brain; MEDLINE=98225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189; MEDLINE=98225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related serine protease.";
J. Biol. Chem. 273:11189-11196(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
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SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE=Ref.4.
MM=26229; METHOD=MALDI; RANGE=33-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Expressed specifically in the limbic mouse brain and is localized at highest concentration in neurons of the highocampal CA1-3 subfields.

MASS SPECTROMETRY: MM-26613; METHOD-MALDI; RANGE=29-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
ENZYME REGULATION: Strongly inhibited by diisopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subtamily.
D30785; BAA06451.1; -.
AB032202; BAA92435.1; -.
BC055895; AAH55895.1; -.
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Kawabe A., Shiosaka S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family. Kallikrein
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PRINTS; PR00772; CHYMOTRYPSIN.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                 TURN
                                                                                                                                                                                                                                                                                                              3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                            interPro;
  62
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                    ហ
                                                                                                                                                                                                                                                                                                            protease;
                                   Similarity
HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRV
         IFLLLCV----LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
                                                                                                                                                                                                                                                                                                                                          IPR001254; Peptidase S1.
IPR001314; Peptidase S1A.
                             Conservative
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140
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Potential.
                             28;
                            Score 622.5;
Pred. No. 5.6e
28; Mismatches
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                                               BE5F6F6BE37CD60E CRC64;
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InterPro; IPR001034; PeptIdase_S1.
InterPro; IPR001254; PeptIdase_S1.
InterPro; IPR001254; PeptIdase_S1A.
InterPro; IPR001314; PeptIdase_S1A.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
R PROSITE; PS00124; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN HIS; 1.
R PROSITE; PS00134; TRYPSIN_SER; 1.
R PROSITE; PS00135; TRYPSIN_SER; 1.
Glycoprotein; Hydrolase; Serine protease; Signal; Zyr
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat Meuropsin precursor (EC 3.4.21.-) (NP) (Kal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ005641; CAA06643.1; -. HSSP; Q61955; 1NPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Fischer; TISSUE=Brain;
MEDLINE=98389725; PubMed=9722524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Klk8; Synonyms=Bsp1, Nrpn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
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) (Kallikrein
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(By similarity).
(By similarity).
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Q9UBX7; O75837; Q9S65;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Kallikrein 11 precursor (EC 3.4.21.-) (Hippostorotease) (UNQ649/PRO1279).

Name=KLK1; Synonyms=PRSS20, TLSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                         Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Hippocampus;
MEDLINE=98438738; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;
Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
"CDNA cloning and expression of a novel serine protease, TLSP.";
Biochim. Biophys. Acta 1399:225-228(1998).
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MEDLINE-20329229; PubMede10872828; DOI=10.1006/bbrc.2000.2761;
MISTAINE-20329229; PubMede10872828; DOI=10.1006/bbrc.2000.2761;
MISTAINE-20329229; PubMede10872828; DOI=10.1006/bbrc.2000.2761;
MISTAINE-2032929; PubMede110.1006/bbrc.2000.2761;
MEDLINE-2032929; PubMede110872929; DOI=10.1006/bbrc.2000.2761;
MEDLINE-2032929; PubMedline-2032929; PubMed
                                                                                           "Genomic organization, mapping, tissue expression, and hormor regulation of trypsin-like serine protease (TLSP PRSS20), a of the human kallikrein gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20130117; PubMed-10662548;
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   SEQUENCE FROM N.A.
                                                                                                                                                                                                Yousef G.M., Scorilas A., Diamandis E.P.;
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                                                                      63:88-96 (2000)
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N-linked (GlcNAc.
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Pred. No. 6.
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                                                                                                                                                                                                                                       DOI=10.1006/geno.1999.6072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
(Hippostasin) (Trypsin-like
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RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Lamerdin J.E., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,
RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Popkie A.P., DeJong P., Dickson M., Gordon D., Eichler E.E.,
Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Robins M. M., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Robins M. M., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
                                                                                                                                                             RX MEDILINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; AS trausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Rx Strausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Rx Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Rx Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Rx Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rx Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rx Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rx Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rx Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Perange C., Rx Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Raheseley R.W., Touchman J.W., Green E.D., Dickson M.C., Raheseley R.W., Touchman J.W., Green E.D., Dickson M.C., Raheseley R.W., Touchman J.W., Shevchenko Y., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human "Generation and initial analysis of more than 15,000 full-length human and manuse C.N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P. Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rubin E.M., Lucas S.M.; "The DNA sequence and biology of human chromosome Nature 428:529-535(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The secreted protein discovery effort to identify novel human s bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cluster
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
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mouse cDNA sequences."; Or more than 15 c. Natl. Acad. Sci. U.S.A. 99:16899-16903 (200: FINCTION: Possible multifunctional protease bz-Phe-Arg-4-methylcoumary1-7-amide, a kallil weakly cleaves other substrates for kallikrei SUBCELLULAR LOCATION: Secreted.
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kallikrein and
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ALTERNATIVE PRODUCTS: Event=Alternative spl

splicing; Named isoforms=2;

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                                                                                                                             Matches
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GO; GO:0008236; F:serine-type peptidase activity; TAS.
GO; GO:0008236; P:serine-type peptidase activity; TAS.
InterPro; IPR009003; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             H-InvDB; HIX0015375; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.257; -. Genew; HGNC:6359; F
                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOId=Q9UBX7-2; Sequence=VSP 005402;
-!- TISSUE SPECIFICITY: Expressed in brain;
1 is expressed preferentially in brain;
-!- SIMILARITY: Belongs to the peptidase S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9UBX7-1;
                                                                        Similarity
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV
                   LQLILLALATGLVGGET-RIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
                                     LSIFLLLCVLGLSQAATPK|FNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                      250
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                                                                       45.0%;
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                                                                                                     MW;
                                                            35;
                                                          Score 618.5;
Pred. No. 1.1e
35; Mismatches
                                                                                                                                                                                                                                          Charge relay system Charge relay system Charge relay system
                                                                                                (in isoform 2).
/FTId=VSP 005402.
192D910BBCDC7A56 CRC64;
                                                                                                                                                                                                                                                                         Activation peptide Kallikrein 11.
                                                                                                                              MQRLRWLRDWKSSGRGLTAAKEPGARSSPLQAM
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d (GlcNAc...) (

d (GlcNAc...) (

ed (GlcNAc...)
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                                                                      5; DB 1;
1.1e-41;
                                                            ; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skin and prostate. Isoform isoform 2 in prostate. family. Kallikrein
                                                                                                                                                                                                                                                                                                                 Serine
                                                                                                                                                                                                                                           (By similarity).
(By similarity).
(By similarity).
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InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009013; Peptidase S1A.
InterPro; IPR009003; Pepti Ser Cys.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Protease; Serine protease.
SEQUENCE 255 AA; 28078 MW; A040914ABC8FF
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Q7JIG6;
05-JUL-2004
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: Belongs to peptidase family SI
EMBL; AF173845; AAS45302.1; -.
HSSP; P00761; 1AKS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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GO:0004263; F:chymotrypsin activity; IEA.
GO:0008233; F:peptidase activity; IEA.
GO:0004295; F:trypsin activity; IEA.
GO:0004295; P:proteolysis and peptidolysis;
             138
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VVSGWGLVSHNEPGTTGRPQSQVSLPDTLHCANISIISDASCDKNYPGRLTNTMVCAGAE
                                                                                                                                          DMTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRVRVTSSVQPLPLPNDCATAGTEC
                                                 HVSGWGITNH-----PRN--PFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGV 190
                                                                                             DGPEQLRTASRVIPHPRY--EARSHRHDIMLLRLVQPARLTPQVRPVVLPTRCPHPGEAC
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larity 49.4%; Pred. No. 4.60
Conservative 31; Mismatches
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Primates; Platyrrhini; Callitrichidae; Saguinus.
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No. 4.6e-41;
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rin: molecular cloning
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Q63ZF2;
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Glandular kallikrein 1
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Q8CGR4;
01-MAR-2003
01-MAR-2003
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Olsson A.Y., Lilja H., Lundwall A.;
"Taxon-specific evolution of glandular kallikrein genes and identification of a progenitor of prostate-specific antigen.";
Genomics 84:147-156(2004).
--- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
EMBL; BK001364; DAA05600.1; -.
                                                                          Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
  SEQUENCE FROM N.A
                                   NCBI_TaxID=10090;
[1]
                                                                                                                                                                      Name=Klk15; Synonyms=KLK15;
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(TYENMBLrel 28, Last sequence up
(TYENMBLrel 28, Last annotation
llikrein 11 precursor.
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                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                           (Mouse)
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250 g
27630 MW;
                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.4%;
                                                                                                                                                                                                                      23,
26,
                                                                                                                                                                                                                         Created)
Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 610; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
glandular kallikrein 11.
; 247B29D3F0DEF8F1 CRC64;
                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; I
Sciurognathi; Muridae;
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nes 90;
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                                                                                                                Euteleostomi;
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                                                                                      Murinae;
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Q8IXD7
     RRACOCCO OG DIT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1
PROSITE; PS00134; TRYPSIN HIS; UI
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; PS00135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Adams M., Mural R.;
Submitted (SEP-2002) to
  Nakamura T., Mitsui
Submitted (JAN-2002)
                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                            Name=KLK11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to permet; AY152434; AAN78422.1; HSSP; P00760; 1EZX.
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                                                  TISSUE=Prostate;
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys.
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                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.297; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178
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     ) s . ,
                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.3%;
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  i T., Yamaguchi N.;
EMBL/GenBank/DDBJ
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QBIXD7 PRELIMINARY; PRT; 2/5 km.
QBIXD7;
QBIXD7;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation updat)
Variant form hippostasin/KLK11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:2447533; Klk15.
GO; GO:0004263; F:chtymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olsson A.Y., Lundwall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHGVYPGRITSNMVCA----GGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 608; DB 2;
Pred. No. 7.9e-41;
0; Mismatches 77
                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299:305-311 (2002)
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databases
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Q6ISIO ID Q6ISIO
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Best Local S
Matches 121
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InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6ISIO PRELIMINARY; PRT; 255 AA.
Q6ISIO;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation updat
Kallikrein 15, isoform 4 preproprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                        TISSUE=PCR rescued clones;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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p; p00760; IEZX.
GO:000423; F:chymotrypsin activity; IEA.
GO:0008233; F:peptidase activity; IEA.
GO:0004295; F:trypsin activity; IEA.
GO:0006508; P:proteolysis and peptidolysis;
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275 AA; 30165 MW; 257A42B28F40B2C4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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Best Local :
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept Ser_Cys.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN 1.
PROSITE; PS500134; TRYPSIN_HIS; UNKNOWN 1.
                                                                                                                                        KLKF HUMAN STANDARD; PRT; 256 AA. 09H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HBG9; 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Kallikrein 15 precursor (EC 3.4.21.-) (ACO prote
                                                                                                                                                                                                                                          HUMAN
   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AN PubMed=11010966; DOI=10.1074/jbc.m005432200; Yousef G.M., Scorilas A., Jung K., Ashworth
                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                              NCBI_TaxID=9606;
                                                                                                               Homo sapiens (Human).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Butte Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2004) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Director MGC Project;
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                                                                                                                                                                                                                                                                                                                                                                                                                          VRPAVLPTRCPHPGEACVVSGWGLVSHNEPGTAGSPRSQVSLPDTLHCANISIISDTSCD
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                                                                                                                                                                                                                                                                                                       KVCHYLEWIRETMKRN
                                                                                                                                                                                                                                                                                                                                    YICKYVDWIRMIMRNN
                                                                                                                                                                                                                                                                                                                                                               KSYPGRITNTMVCAGAEGRGAESCEGDSGGPLVCGGILQGIVSWGDV-PCDNTTKPGVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQPLPLPNDCATAGTECHVSGWGITNH------PRN--PFPDLLQCLNLSIVSHATCH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSRFMRVRLGEHNLRKRDGPEQLRTTSRVIPHPRY--EARSHRNDIMLLRLVQPARLNPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLCVLGLSQAAT----PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease; Serine protease 255 AA; 28016 MW; 1581B
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                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.6%; Score 599; DB 2;
46.9%; Pred. No. 4.2e-40;
cive 32; Mismatches 86
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peptidase family S1.
                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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(ACO protease).
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                                  SPECIFICITY
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A., Schein J.
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    E.P.;
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В. У.
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MEROPS; S01.081; -..

Genew; HGNC:20453; KLK15.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0004252; F:serine-type endopeptidase activity; NAS.

GO; GO:0004252; P:serine-type and peptidolysis; NAS.

InterPro; IPR009003; Peptidase Cys.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
                                                                                                                                                                                                                                  EMBL; AF242195; AAG09469.1; -.
EMBL; AF242195; AAG09470.1; -.
EMBL; AF242195; AAG09471.1; -.
EMBL; AF242195; AAG09472.1; -.
EMBL; AF242195; AAG09472.1; -.
EMBL; AF243527; AAG33354.1; -.
EMBL; X75363; CAA53145.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                   entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8; Hillman R.T., Green R.E., Brenner S.E.; "An unappreciated role for RNA surveillance."; Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).-!- FUNCTION: Protease whose physiological substration SUBCELLULAR LOCATION: Secreted (Probable).-!- ALTERNATIVE PRODUCTS;
   PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                   modified
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dihanich M.E., Spiess M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11054574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning
                                                                                                                                                                                                                                                                                                                                                e European Bioinformatics Institute. There are no restrictions on its e by non-profit institutions as long as its content is in no way diffied and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId-Q9H2R5-4; Sequence-VSP_005404; TISSUE SPECIFICITY: Highest expression in the thyroid glame expressed in the prostate, salivary, and adrenal glands and colon testis and kidney.

SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event-Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257:119-130(2000).
                                                                                   PF00089; Trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9H2R5-2; Sequence=VSP 005405;
Note=May be produced at very low levels due to a premature codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9H2R5-3; Sequence=VSP_005406,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    soId=Q9H2R5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Paeper B., Wang K.; cing and expression analysis located in chromosome 19q13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine proteinase-like sequence
Biophys. Acta 1218:225-228(1994)
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Smith R., Argonza-Barrett R., Lei H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;
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Best Local S
Matches 121
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SIGNAL
                                                              MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2; Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.; "cDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRSS20).";
Yamaguchi N., Mitsui S.;
Submitted (JUL-1998) to the
-!- SIMILARITY: Belongs to
                                                                                                                                                                                     01-MAY-2000
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                          TISSUE=Brain;
                                    SEQUENCE FROM N.A.
                                                                                                               SEQUENCE
                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                   Hippostasin.
Name=2310015I08Rik;
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Rodentia;
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          the EMBL/GenBank/DDBJ databases
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/FTId=VCT
peptidase
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Activation pe
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Charge relay
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2; Mismatches
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SHNEPGTAGSPRSQ ->
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/FTId=VSP
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/ -> G (in isofo
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No. 4.2e-40;
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RESULT 15
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GO; GO:0005615; C:extracellular space
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009031; Pept Ser_Cys.
Pfam; PP00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                 TISSUE=Prostate;
MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hippostasin full-length serine, 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9QYN3
Q9QYN3;
01-MAY-2000
01-MAY-2000
                                           TISSUE=Prostate;
Yamaguchi N., Mitsui
                                                                                                                                                           Mitsui S., Okui A., Kominami K., ("CDNA cloning and tissue-specific hippostasin/TLSP (PRSS20).";
                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
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Name=2310015I08Rik;
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SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
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RIKEN full-length enriched library,
act:protease, serine, 20, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 28, Last sequence update)
(Premblrel. 28, Last annotation update)
(prostate type (Mus musculus adult male tongue cDNA, RI
enriched library, clone:2310015108 product:protease,
enriched library, clone:2310014080707
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                   EMBL/GenBank/DDBJ databases
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Pred. No. 5.
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Matsuyama T., Miyazaki A., Nishi K., Noura K., Numazaki R., Ohno M.,
A Matsuyama T., Miyazaki A., Nishi K., Noura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Shinagawa A., Shiraki T.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sayabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
A Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBI/GenBank/DDBJ databases.

- !- SIMILARITY: Belongs to peptidase family S1.

EMBI, AK009720; BAB26241.2; -.

EMBI, AK009720; BAB26461.2; -.

BEBL; AK09720; BAB26461.2; -.
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RC STRAIN=C57BL/6J; TISSUE=Tongue;

RC STRAIN=C57BL/6J; TISSUE=Tongue;

RMEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RMEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RMEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Watahiki M.,

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RRI "RIKEN integrated sequence analysis (RISA) system-384-format

RE sequencing pipeline with 384 multicapillary sequencer.";
                                                    MGD; MGI:1929977; 2310015108Rik.
GO; GG:0005615; C:extracellular space;
InterPro; IPR001254; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001303; Pept Ser Cys.
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STRAIN=C57BL/6J; TISSUE=Tongue;

MEDLINE=2049974; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

Canninci P., Shibata Y., Muramatsu M., Hayashizaki Y.;

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

"Normalization and subtraction of cap-trapper of new genes.";
                    Pfam; PF00089; Trypsin; PRINTS; PR00722; CHYMOTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
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Nature 420:563-573(2002).
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STRAIN=C57BL/60; TISSUE=Tongue;

MEDLINE=99279253; PubMed=10349636; DOI=10.10

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
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MEDLINE=21085660; PubMed=11217851;
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; P00760; 1E
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                    CHYMOTRYPSIN.
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Search completed: March 5, 2005, 18:20:29 Job time : 178 secs
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PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;
                                              266 FNWIHEVMRNN 276
                                                                                          207 NITDTMLCASVRKEGKDSCQGDSGGPLVCNGSLQGIISWGQ-DPCAVTRKPGVYTKVCKY 265
                                                                                                         179 RITSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTVICKY 237
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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GEN

TITLE OF INVENTION: WITH HUMAN DISBASE, METH

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESTSEQ for Windows Version 4.0

SEQ ID NO 8151

LENGTH: 249

TYPE: PRT

ORGANISM: Human

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; Patent No. 6812339
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Pred. No. 3.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                .5; DB 4;
3.1e-124;
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OF DETECTION AND
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249; 1,

Gaps

241 240 181 180 121 120 62 USES

THEREOF

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APPLICANT: Ni, et al.

APPLICANT: Ni, et al.

FILE REFERENCE: PF391

CURRENT APPLICATION NUMBER: US/09/244,111

CURRENT FILING DATE: 1999-02-04

EARLIER APPLICATION NUMBER: 60/073,961

EARLIER APPLICATION NUMBER: 60/073,961

EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-244-111-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
VIMMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 6948
LENGTH: 254
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US-09-244-111-6
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; ORGANISM: Human
US-09-949-016-6948
                                                                                                                                                        Matches
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Applicat Patent No. 6566498 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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19
                                   61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
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                                                                          MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                               MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA 60
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                                                                                                                                                        Conservative
                                                                                                                                                                         59.0%;
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                                                                                                                                                    Score 811; DB 4; Length 162; Pred. No. 3.8e-71; O; Mismatches 3; Indels
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RESULT 4

US-09-618-259-7

; Sequence 7, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013e1
; TITLE OF INVENTION: No. 6642013e1
                        ; Sequence 2, Application US/09070526
; Patent NO. 6100059
; GENERAL INFORMATION:
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: CLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
TITLE OF INVENTION: NO. 6100059el Co
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: DEPORTED E DEPORTED
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SEQ ID NO 7
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CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 260
TYPE: PRT
ORGANISM: Homo sapiens
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                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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P.O.
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                  RATNER & PRESTIA
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d, Lowell J.
No. 6642013el Extracellular Serine Protease
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Pred. No. 2.5e-53;
4; Mismatches 93
                                                                    Compounds
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US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136
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// MOLECULE TYPE: protein
us-09-070-526-2
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Best Local Similarity
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APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-JUN-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/ACENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEPHONE: 610-407-0701
                                                      GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO:
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SOFTWARE: FASTSEQ for I
CURRENT APPLICATION DATA:
                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STATE: F
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 30-APPLICATION:
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                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
                                                                                                                                                                                                                                                                                                                                                                                                                              133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQI 192
                                                                                                                                                                                                                                                                              252
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 3: Incyte Pharmaceuticals,
3174 Porter Dr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.6%; Score 626.5; DB 3; 50.4%; Pred. No. 6.2e-53; tive 23; Mismatches 92;
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                                                                                                                                                                                                                        RESULT 7
                                                                                                                           Sequence 7, Application US/09008271A Patent No. 6203979
PATENT INFORMATION:
APPLICANT: Bandman, Olga
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECHRONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: GELLETONE: 1020091
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STATE: CA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/025,059
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 TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ILLLIFMGAWAGLTRAQGSKILEGRECIPHSQPWQAALFQGERLICGGVLVGDRWVLTAA 72
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Tang, Tom Y.
Shah, Purvi
INVENTION: HUMAN PROTEASE MOLECULES
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                              Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
                                                                                                              Hillman, Jennifer L.
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Pred. No. 1.5e-52;
?8; Mismatches 93;
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Indels Length 260;

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Gaps

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US-09-618-259-8
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                    Sequence 8, Application US/09618259
Patent No. 6642013
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: No. 6642013e1 Extracellular Serine
FILE REFERENCE: D6020CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 122;
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CURRENT APPLICATION NUMBER: US/09/618,259
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CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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RMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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ATTORNEY AGENT INFORMATION:
NAME: Wohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
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TYPE: amino acid
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ilarity 49.8%;
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Pred. No. 1.5e-52;
4; Mismatches 94
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60/048,964

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US-09-205-258-427
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-618-259-8
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CURRENT FILING DATE: 1998.12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ0077P1
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                                                                                                                                                                                                                                                                                                                        ER APPLICATION NUMBER: 60/048,881
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,880
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,896
ER FILING DATE: 1997-06-06
ER FILING DATE: 1997-06-06
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                                                              FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
                                                                                                                                                                                                                          APPLICATION NUMBER: 60/048,895
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/048,876
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/049,375
FILING DATE: 1997-06-06
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Pred. No. 1.5e-52;
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NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 427
LENGTH: 250
TYPE: PRT
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Local Similarity 48.2%;
hes 120; Conservative
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APPLICATION NUMBER: 60/092,921
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FILING DATE: 1997-06-06
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Pred. No. 3.5e-52;
05; Mismatches 89;
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US-09-025-059-1
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                                                                                                             Matches
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APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Well C.
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SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
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                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
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                                                                                                                                                                          Local Similarity
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CITY: Palo Alto
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48.2%;
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                                                                                                             35;
                                                                                                          Score 618.5; DB 3;
Pred. No. 4.1e-52;
5; Mismatches 89;
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                                                                                                             Indels
                                                                                                                                          Length 282;
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                                                                                                             Gaps
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APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                       US-09-386-642-14
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                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                    Sequence 14, Application US/09386642 Patent No. 6420157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Symogen Activation
FILE REFERENCE: ORT-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: with homo sapien serine protease catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                        ECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPGQDACQG
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51.1%;
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Pred. No. 1.5e
21; Mismatches
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ches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: STEWART, APPLICANT: STROUPE, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: with homo sapien serine protease catalytic
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                               NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park
                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application
                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
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                                                                                                                                                         424
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AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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Pred. No. 3.8e-50;
4; Mismatches 79
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US
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Sequence 2, Application US
PATENT NO. 5945328
GENERAL INFORMATION:
APPLICANT: WOLDIKE, He
APPLICANT: KJELDSEN, T
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US-08-956-267A-2
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
                                                             TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CATOl
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4500
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
OPERATING SYSTEM: DOS
SOFTWARE: FASTERO for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 248 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 62324
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WOLDIKE, Helle Fabricius APPLICANT: KJELDSEN, Thomas Borglum TITLE OF INVENTION: A Process For PaTITLE OF INVENTION: (Trypsinogen)
                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
LENGTH: 24, ....
THOSE; amino acid
                                                                                                                                                                                    APPLICATION NUMBER: US/0
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
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                             247 amino acids
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IBM Compatible
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47.8%; Pred. No. 3.9e-50;
tive 36; Mismatches 87;
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; ORGANISM: Human US-09-949-016-8166
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US-09-949-016-8166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8166
LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Patent No. 6812
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Matches 113; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                180
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210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
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                                                                                                                                                                                                                                                                                                                                                                                               116;
                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                       13 GLSQAATPKIFN------GTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 HCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNG--NTLDNDIMLIKLSSPATLN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ហ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6812339
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                                         ITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYV 238
                                                                                                                                     TSSVQPLPLP-NDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR 179
                                                                                                                                                                                                                                                                                                GVSQESS-KVLNTNGTSGFLPGGYTCFPHSQPWQAALLVQGRLLCGGVLVHPKWVLTAAH
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  ITDNMLCAGTKEGGKDSCEGDSGGPLVCNRTLYGIVSWGDF-PCGQPDRPGVYTRVSRYV
                                                                                                                                                                                              CLKEGLKVYLGKHALGRVEAGEOVREVVHSIPHPEYRRSPTHLNHDHDIMLLELQSPVQL 149
                                                                                                                                                                                                                                            CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST -- SHEHDLRLLRLRLPVRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRMIMRNN 248
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                                                                                            TGYIQTLPLSHNNRLTPGTTCRVSGWGTTTSPQVNYPKTLQCANIQLRSDEECRQVYPGK
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46.8%; Pred. No. 4.4e-47;
ative 36; Mismatches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 290;
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                                                                                                 209
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Search comp Job time :	Db	Q
Search completed: March 5, 2005, 18:16:40 Job time : 46 secs	269 LWIRETIR 276	239 DWIRMIMR 246
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RESULT
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Maximum DB seq length: 200000000
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                                                                                                                                                                     AAY99393 standard; protein; 248 AA.
Human PRO1303 (UNO669) amino acid s
WO200012708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB21304 standard; protein;
Human KLK-L5 protein #4.
WO200053776-A2.
                                                                      AAM23994 standard;
Human EST encoded p
WO200154477-A2.
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14-SEP-2000.
(GETH ) GENENTECH INC.
(GETH ) 100.0%;
(GETH ) 100.0%;
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                                                           02-AUG-2001
                                                                                                                                                                                                                                                                                AAB24032 standard; protein; 248 AA.
Human PRO1303 protein sequence SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000
 AAB66142 standard;
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14-SEP-2000.
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                                               (HYSE-) HYSEQ INC.
                                                                                                                                                  (GETH )
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No. is the number of results predicted by chance to have greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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Similarity 100.0%;
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I geneseqp1980s:*
2 geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001as:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
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1374
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protein;
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                                                                                    n; 248 AA.
SEQ ID NO:
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Pred.
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Pred.
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Pred.
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No. 5e
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No. 5e-98;
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No. 5e-98;
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Best Local Similarity
RESULT 12
ID ADD39786 standard; pr
DE Human secreted/transm
PN US2003083462-A1.
PD 01-MAY-2003.
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ID ABO4
DE Huma:
PN US20
PD 06-M
                                                                                                            Best Loc
RESULT 14
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RESULT
 Best Local Similarity
RESULT 15
ID ADD39309 standard;
DE Human secreted/tran
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RESULT 13
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Best Local Similarity
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Human secreted/transmembrane
US2003099625-A1.
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ADD39309 standard; protein; 248 AA.
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Human secreted/transmembrane protein PRO1303.
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15-MAY-2003.
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Human secreted/transmembrane
US2003224478-A1.
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Human secreted/transmembrane protein PRO1303.
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Best Local Similarity
RESULT 34
                                                       Best Local Similarity
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                       ABG66676 standard; protein; Human novel polypeptide #11. WO200244340-A2.
                                                                                                                                                                                                                                                   AAB21303 standard; protein;
Human KLK-L5 protein #3.
WC200053776-A2.
                                                                                                                                                                                                                                                                                                                               AAO29516 standard; protein; 248 AA.
Human kallikrein-like protein 5 (18817).
WO2003039475-A2.
                                                                                                                                                                                                                                                                                                                                                                                         AU2003259607-A1.
27-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                            Human kallikrein 12,
WO2004029285-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH61514 standard; protein; 2
Human secreted/transmembrane
US2004014130-A1.
       Human PRO protein
WO2004039956-A2.
13-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                     ADT94373 standard; protein;
Human PRO1303 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL94713 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN10927 standard; p
Human kallikrein 12,
WO2004029285-A2.
                                    ADP56174 standard;
                                                                Y MATCH SINAI HOSPITAL.

Y Match 94.7%;
                                                                                    08-APR-2004.
                                                                                                                ADN10926 standard;
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                                                                                                                                                    (HYSE-) HYSEQ INC.
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th 100.0%;
Similarity 100.0%;
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                          ; protein;
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. No. 2.2e-92;
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. No. 2.2e-92;
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No. 1.
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No. 5e-98;
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No. 5e-98;
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No. 5e-98;
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.2e-92;
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Best L.
RESULT 51
ID AAUJ
DE Hur
PN V
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RESULT 48
ID AAB21322 standard; p
DE Human neuropsin.
PN W0200053776-A2.
PD 14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
RESULT 49
ID AAB44300 standard; p
DE Human PRO322 (UNQ283
PN W0200053756-A2.
PD 14-SEP-2000.
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RESULT 46
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RESULT 44
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RESULT 43
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Best Local Similarity
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                                                                                   24-NOV-1993.
(SHIO/) SHIOZAKA S.
(SHIO/) SHOZAKA S.
(SHIO/) SEIBUTSUGAKU KENKYUSHO KK.
45.9%; SCOTE 630.9
24-NOV-1993.
45.9%; SCOTE 630.9
25.2%; Pred. No.
                                                                                                                                                                                    Human neuropsin protein. JP11318461-A. 24-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY03220 standard; protein; Amino acid sequence of human W09909138-A1.
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(GETH ) GENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOUN ) MOUNT SINAI
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16-SEP-1999.
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Human secreted protein from
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                           WO200140466-A2.
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                                                 Human PRO322
                                                                  AAU12369 standard;
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(UNQ283) protei
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45.9%;
50.2%;
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cDNA clone HKAFV61.
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No. 1.1e-40;
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No. 1.1e-40;
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1.1e-40;
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.2e-92;
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.5e-71;
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GENENTECH INC

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RESULT 57
       Best
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RESULT 52
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Best Local
                                                              Novel human secreted and tra
US2003032156-A1.
                                                                                                                                                                                                                    ADI17076 standard;
Human NOVX protein
WO200268649-A2.
                                         (GETH )
                                                            L3-FEB-2003
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WO200208284-A2.
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WO200109327-A2.
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Human PRO322 protein sequenc
WO200200690-A2.
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(GETH ) GENENTECH
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Novel human diagnostic protein #23364.
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STEPHAN J F.
WATANABE C K.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                  CURAGEN CORP.
                                       GENENTECH INC.
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PAONI
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BAKER K P.
FERRARA N.
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GERRITSEN M E.
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Best Local Similarity

RESULT 61

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RESULT 60
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RESULT 62
ID ADA05702 standard; px
DE Human NOV11h protein
PN W02003029424-A2.
PD 10-APR-2003
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Novel secreted and t
US2003017563-A1.
23-JAN-2003.
                                    ABO25038 standard; protein; 2
Human secreted/transmembrane
US2003036179-A1.
20-FEB-2003.
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US2002169284-A1.
14-NOV-2000
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Human secreted and
US2002177553-A1.
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Human PRO polypeptide #198.
US2003036180-A1.
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ABU80399 standard; protein; 260 AA.

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U$2003073212-A1.
17-APR-2003.
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Human PRO polypeptide #198.
US2003082704-A1.
01-MAY-2003.
                                                                                                                                                                                                                                                                               Homo sapiens.
US2003049816-A1.
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                                                        ADA86424 standard; protein; 260 AA. Novel human secreted and transmembrane US2003082711-A1.
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Best Local Similarity
RESULT 80
ID ADB30576 standard; p1
DE Human PRO polypeptide
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC
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Best Local Si
RESULT 81
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RESULT 79
RESULT 86
ID ADA91
DE Novel
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                                                                                                                                  Novel human secreted and transmembrane US2003087345-A1.
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                                                           Human PRO polypeptide #198.
US2003087349-A1.
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US2003087350-A1.
08-MAY-2003.
ADA91821 standard; protein; 260 AA. Novel human secreted and transmembrane
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(GETH ) GENENTECH
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Human PRO polypeptide #198.
US2003068795-A1.
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No. 1.1e-40;
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protein PRO322

US2003082694-A1

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Query Match
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RESULT 91
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RESULT 93
ID AB043346 standard; p
DE Novel human secreted
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH IN
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01-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.9%; /
ADA12595 standard; protein; ; Human secreted/transmembrane US2003055216-A1.
                                                                                                                                              ABO19701 standard; protein; 260 AA. Novel human secreted and transmembrane US2003050240-A1.
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US2003082710-A1.
01-MAY-2003
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Human PRO polypeptide #198.
US2003077722-A1.
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(GETH ) GENENTECH INC.
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RESULT 98
ID ADA82279 standard; p
DE Human PRO polypeptid
PN US2003082701-A1.
PD 01-MAY-2003.
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RESULT 103
ID ADAPATT
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ID AD
DE No
PN US
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ID ADA75
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US2003073214-A1.
17-APR-2009
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01-MAY-2003.
(GETH ) GENENTECH INC.
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US2003082695-A1.
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Human PRO polypeptide #198.
US2003073216-A1.
17-APR-2003.
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(GETH ) GEN
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US2003077713-A1.
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Human PRO polypeptide #198.
US2003068798-A1.
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Human PRO polypeptide SEQ ID
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(GETH ) GENI
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No. 1.1e-40;
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1.1e-40;
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Best Local Similarity
RESULT 113
ID ADAS1104 standard; p)
DE Human PRO polypeptide
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 111
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RESULT 107
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US2003049817-A1.
13-MAR-2003.
(GETH ) GENENTECH I
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US2003082690-A1.
01-MAY-2007
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US2003096386-Al.
22-MAY-2007
            Human PRO polypeptide #198. US2003082702-A1.
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US2003077721-A1.
24-APR-2007
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US200307310-A1.
17-APR-2007
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Human PRO polypeptide #198.
US2003092147-A1.
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Human PRO polypeptide SEQ II
US2003077715-Al.
24-APR-2003.
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RESULT 117
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RESULT 120
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01-MAY-2003.
(GETH ) GENENTECH INC.
45.9%; /
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US2003049633-A1.
                                       ADA46467 standard; protein; Novel human secreted and tru
US2003054516-A1.
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Human PRO polypeptide #198.
US2003077710-A1.
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01-MAY-2003.
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RESULT 124
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Novel human secrete
US2003087344-A1
08-MAY-2003.
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ADB23651 standard; protein;
Human PRO polypeptide SEQ I
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Human PRO polypeptide #198.
US2003022239-A1.
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US2003082686-A1.
01-MAY-2003
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US2003059909-A1.
27-MAR-2003.
                                             (GETH ) GENENTECH INC.
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US2003082699-A1.
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US2003073213-A1.
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Human PRO polypeptide #198.
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protein

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Best Local Similarity RESULT 141
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RESULT 136
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Best Local S
RESULT 134
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Best Local
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Novel human secreted and transmembrane US2003082764-A1.
                                                                  ADB80561 standard; protein;
Ovarian cancer-associated px
WO200210235-A2.
27-DEC-2002.
(EOSB-) EOS BIOTECHNOLOGY IN
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01-MAY-2003.

(GETH ) GENENTECH INC.

45.9%;

MATCH 13-TITY 50.2%;
                                                                                                                                                             ADB90420 standard; protein;
Human PRO polypeptide #198.
US2003082762-A1.
01-MAY-2003.
                                                                                                                                                                                                                                                       ADB89688 standard; protein;
Human PRO polypeptide #198.
US2003082698-A1.
                                                                                                                                                                                                                                                                                                                                     ADB66608 standard; protein;
Novel human secreted and tra
US2003082689-A1.
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US2003087347-A1.
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ry Match 45.9%;
t Local Similarity 50.2%;
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Novel human secreted and tra
US2003082766-A1.
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(GETH ) GENENTECH INC.
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US2003082712-A1.
01-MAY-2003
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24-APR-2003.
(GETH ) GENENTECH INC.
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) GENENTECH INC.
45.9%; 50.2%;
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                                           BIOTECHNOLOGY INC.
45.9%; Score
ilarity 50.2%; Pred.
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45.9%;
y 50.2%;
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transmembrane
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No. 1.1e-40;
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No. 1.1e-40;
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Query Match
Best Local Similarity
RESULT 150
ID ADB35065 standard; p
DE Human PRO polypeptid
PN US2003077718-A1.
PD 24-APR-2003.
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Human PRO polypeptide SEQ ID NO 396. US2003077718-A1. 24-APR-2003.
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US2003082687-A1.
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Human PRO polypeptide #60.
US2003083248-A1.
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Best Loca
RESULT 153
Best Local Similarity
RESULT 159
ID ADC68116 standard; p
DE Human secreted/trans
PN US2003069178-A1.
PD 10-APR-2003.
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Best Local Similarity
RESULT 158
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RESULT 156
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RESULT 151
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Human secreted/transmembrane
US2003068648-A1.
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Human secreted/transmembrane
US2003064407-A1.
03-APR-2003.
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Human secreted/transmembrane
US2003054405-A1.
           Human secreted/transmembrane US2003069178-A1.
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27-MAR-2003.
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Human secreted/transmembrane
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01-MAY-2003.
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polypeptide SEQ ID NO 396.
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ed and transmembrane
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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Best Local Similarity
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Best Local S
RESULT 161
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RESULT 165
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Best Local Similarity
RESULT 160
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RESULT 162
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                                                                                                 Novel human secreted and transmembrane US2003087365-A1.
                                Novel human secri
US2003087366-A1.
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                                                     ADC57324 standard;
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                                                                                              (GETH )
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Human secreted/transmembrane
US2003104998-A1.
                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                    5-MAY-2003
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Human secreted/transmembrane
US2003073624-A1.
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17-APR-2003.
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RESULT 173
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                                       ADD03221 standard; protein; Novel human secreted and trauscoos 092104-A1.
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08-MAY-2003.
                                                                                                                                   Novel human
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                                                                                                                                            ADC58547 standard;
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US2003087362-A1.
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Local Similarity

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RESULT 178

ID ADC90213 standard; protein; 260 AA.

DE Novel human secreted and transmembrane
PN US2003087348-A1.
PD 08-MAY-2003.
                                                                 Best Local Similarity RESULT 186
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RESULT 183
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16-OCT-2003.

(GETH ) GENENTECH INC.

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Human PRO polypeptide #198.
US2003194774-A1.
                                    Human secreted/transmembrane US2003105011-A1.
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Human kallikrein 8
WO2003085404-A1.
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Novel human secreted and transmembrane
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08-MAY-2003.
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Human PRO polypeptide #198.
US2003194776-A1.
                                                         ADD10361 standard; protein;
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RESULT 191
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US2003087358-Al.
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                                                                                                                              Novel human secreted and transmembrane US2003203437-A1.
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US2003203438-A1.
                                                                 ADD37114 standard; protein; :
Human secreted/transmembrane
                                                                                                                                                                                                                     שניבניים standard; protein;
Human PRO polypeptide #198.
US2003104700 **
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                                                         US2003105012-A1.
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                  Similarity
                                      GENENTECH
standard; protein;
                  45.9%;
50.2%;
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Pred. No. 1.1e-40;
                                                                  polypeptide
                  630.5;
No. 1.1
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No.
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No. 1.1e-40;
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1.1e-40;
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1.1e-40;
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Best Local Similarity
RESULT 203
ID ADD91426 standard; p
DE Human PRO polypeptid
PN US2003199055-A1.
PD 23-OCT-2003.
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Best Local S
RESULT 202
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RESULT 204
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Best Local Similarity
RESULT 199
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RESULT 198
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23-OCT-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.9%; (
Match 19-rity 50.2%;
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Human PRO polypeptide #198.
US2003194779-A1.
16-OCT-2003.
(GETH) GENENTECH INC.
   Novel
                                                                        ADE04040 standard; protein;
Human PRO polypeptide #198.
US2003199057-A1.
                                                                                                                                                Human PRO polypeptide #198. US2003199055-A1. 23-OCT-2003.
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Human PRO polypeptide #198.
US2003199030-A1.
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30-CCT-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.9%; (45.9%; (45.9%; (45.9%))
            ADE32337 standard;
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                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-2003
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30-OCT-2003.
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Human PRO polypeptide #198.
Περορορογίος το
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Human PRO polypeptide #198.
US2003203431-A1.
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secreted and tra
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and transmembrane
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in; 260 AA.
transmembrane
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No. 1.1e-40;
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No. 1.1e-40;
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Best Local Similarity
RESULT 213
ID ADDOORS
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Best Local S
RESULT 214
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RESULT 208
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Best Local Similarity
RESULT 207
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RESULT 206
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ADE33441 standard; protein, Novel human secreted and tra US2003194767-A1.
                                                                Human PRO polypeptide #198. US2003199053-A1. 23-OCT-2003.
                                                                                                                                                   ADE17846 standard; protein;
Human PRO polypeptide #198.
US2003199023-A1.
23-OCT-2003.
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                                                                                                                                                                                                                                                                                                                  ADD73212 standard; protein; ; Human secreted/transmembrane US2003203436-A1.
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30-OCT-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted/transmembrane
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Human secreted/transmembrane
US2003203434-A1.
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30-OCT-2003.
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US2001201470 *1
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16-OCT-2003.
(GETH) GENENTEC
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         in; 260 AA.
transmembrane
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No. 1.1e-40;
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No.
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No. 1.1e-40;
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No. 1.1e-40;
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1.1e-40;
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         protein PRO322.
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. 1.1e-40;
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Ouery Match
Best Local 8'
RESULT 222
ID ADD959'
DE Huma'
PN US'
PD 95
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Query Match
Query Match
Best Local Similarity 50.2*;

RESULT 218

ID ADD72570 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRC pN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
45.9%; Score 630.
PA 45.9%; Score 630.
                                                                                                                                                                                                                                                                           RESULT 220
ID ADE189
DE Human
PN US2003
PD 23-OCT
PA (GETH
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RESULT 221
Query Match 45.9%; Score
Best Local Similarity 50.2%; Pred.
RESULT 23
ID ADE22821 standard; protein; 260 AA.
BE Human PRO polypeptide #198.
PN US2003199064-A1.
PD 23-OCT-2003.
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06-NOV-2003.

(GETH ) GENENTECH INC.

45.9%; S

Match 17artty 50.2%;
                                                                                                                                               US20012203.
23-OCT-2003.
(GETH) GENENTECH INC.
45.9%; /
                                                                                               Human PRO polypeptide #198.
US2003199059-A1.
23-OCT-2003
                                                                                                                                                                                                                                                                                           Human PRO polypeptide #198.
US2003199026-A1.
23-OCT-2007
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US2003199025-A1.
23-OCT-->^^
                                                                                                                                                                                                    ADE43146 standard; protein;
Human PRO polypeptide #198.
US2003199033-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD93082 standard; protein;
Human PRO polypeptide #198.
US2003194768-A1.
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Human PRO polypeptide #198.
US2003207417-A1.
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(GETH) GENENTECH INC.
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Local Similarity 50.2%;
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Pred. No. 1.1
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Pred. No. 1.1e-40;
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No. 1.1e-40;
                                                         630.5; DB 7;
No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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                    Novel human secreted and transmembrane US2003207381-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.9%;
Match 45.9%;
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                                                                                                                                                                                          Human secreted/transmembrane US2003206915-A1.
                                                                                                                                                                                                             ADG60312 standard;
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Human secreted/transmembrane
US2003216561-A1.
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US2003207370-Al.
06-NOV-2003
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06-NOV-2003.
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06-NOV-2003.
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                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
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Novel human secreted and transmembrane protein PRO322.
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and transmembrane
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No. 1.1e-40;
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No. 1.1e-40;
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RESULT 244
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RESULT 246
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SULT 242
                                  Cancer/angiogenesis/fibrosis-related WO2003042661-A2.
                                                                                                                                      Novel human secreted and
                                                                                                                            US2003087385-A1.
                                                                                                                                                ADN16604 standard;
                                                                                                                                                                                                                        ADN15975 standard;
Novel human secrets
                                                                                                                                                                                                                                                                                                       ADM82576 standard; protein; 260 AA. Novel human secreted and transmembrane
                                                                                                                                                                                                             US2003087353-A1.
                                                                                                                                                                                                                                                                             (GETH )
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Novel human secreted and transmembrane
US2003207377-A1.
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Novel human secreted and tra
US2003207385-Al.
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45.9%; (
 EOS BIOTECHNOLOGY INC. h 45.9%; Similarity 50.2%; F
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630.5; DB 7;
No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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                               Human PRO polypeptide #198.
US2003211571-A1.
13-NOV-2003.
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Human PRO polypeptide #198.
US2003100087-A1.
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US2003087357-A1.
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Human PRO polypeptide #198.
US2003092113-A1.
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Novel human secreted and try
US2003207386-Al.
06-NOV-2003.
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15-MAY-2003.
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Novel human secreted and tra
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Human PRO polypeptide #198.
US2003194794-A1.
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Human PRO polypeptide #198.
US2003199062-A1.
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US2003092108-A1.
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Human secreted/transmembrane
US200310497-A1.
29-MAY-2003.
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Human PRO polypeptide #198.
US2003199061-A1.
23-OCT-2003.
                                                                                                  Human PRO polypeptide #198.
US2003199027-Al.
23-OCT-2000
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GODOWSKI P J.
GIRMALDI J C.
GURNEY A L.
HILLAN K J.
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KUO S S.
NAPIER M A.
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DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
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STEWART T A.
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PN US200319437-A1.
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RESULT 282
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16-OCT-2003.
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30-OCT-2003.
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Human PRO polypeptide #198.
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23-OCT-2003.
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RESULT 286
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                                                                     Novel human secreted and transmembrane US2003199058-A1.
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Human secreted/transmembrane
US2003211092-A1.
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Human PRO polypeptide #198.
US2003199063-A1.
23-OCT-2003.
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Human secreted/transmembrane protein,
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ADG02312 standard; protein; Human PRO polypeptide #198.
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Best Local Similarity
RESULT 294
ID ADG22098 standard; p
DE Novel human secreted
PN US2003207360-A1.
PD 06-NOV-2003.
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US2003207422-A1.
06-NOV-2003.
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US2003207353-A1.
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US2003208055-A1.
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        ADG05241 standard; protein;
Human PRO polypeptide #198.
                                                                      ADG16782 standard; protein;
Human PRO polypeptide #198.
US2003207359-A1.
06-NOV-2003.
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Human PRO polypeptide #198.
US2003207376-A1.
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Human PRO polypepti
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Best Local Similarity
RESULT 311
ID ADG24929 standard; p
DE Novel human secreted
PN US2003207427-A1.
PD 06-NOV-2003.
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RESULT 310
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06-NOV-2003.
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Novel human secreted and transmembrane
US2003207389-A1.
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Human PRO polypeptide #198.
US2003207374-A1.
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Human PRO polypeptide #198.
US2003207371-A1.
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27-NOV-2003.
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Human PRO polypeptide #198.
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Novel human secreted and transmembrane
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(GETH ) GEN
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Human PRO polypeptide #198.
US2003207425-A1.
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                            ADG55825 standard;
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Novel human secreted and transmembrane
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US2003207358-A1.
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06-NOV-2003.
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US2003077723-A1.
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(GETH ) GENENTECH TWO
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US2003207805-A1.
06-NOV-2003.
                              Novel human secreted and transmembrane US2003207419-A1.
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                                                      ADG48696 standard; protein; Human secreted/transmembrane
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Human PRO polypeptide #198.
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Human secreted/transmembrane
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1.1e-40;
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J GENENTECH 1

ABST LOCAL Similarity

RESULT 346

ID ADG62592 stand

BHuman secre

PN US20046

PD 08

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                                                                                      Best Local Similarity RESULT 347
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RESULT 343
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RESULT 340
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                                           Human PRO polypeptide #198. US2003207361-A1. 06-NOV-2003.
                                                                                                                               ADG62592 standard; protein; 260 AA. Human secreted/transmembrane protei US2004006219-A1.
                                                                                                                                                                                                          ADG59136 standard; protein; 2
Human secreted/transmembrane
US2004005657-A1.
                                                                                                                                                                                                                                                                                                                                                               ADG51192 standard; protein; 2 Human secreted/transmembrane US2004005312-A1.
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Human PRO polypeptide #36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003207369-A1.
06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG54721 standard; protein; 260 AA. Novel human secreted and transmembrane
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Human PRO polypeptide #198.
US2003022331-A1.
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                  Local Similarity
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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Best Local Similarity
RESULT 355
ID ADI37154 standard; p)
DE Human TADG-14 protein
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 353
ID ADI14731 standard; p
DE Novel human secreted
PN US2003207383-A1.
PD 06-NOV-2003.
                      Best
RESULT
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RESULT 354
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Best Local Similarity
RESULT 352
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RESULT 350
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RESULT 349
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 Human
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04-FEB-2004.
(GETH) GENENTECH INC.
45.9%;
Match 45.9%;
50.2%;
          ADJ77502 standard;
                                                                   26~FEB-2004
                                                                          Novel human secr.
US2004039164-A1.
                                                                                  ADJ63607 standard; protein; 260 AA.
Novel human secreted and transmembrane
                                                                                                                                                                    Human TADG-14 protein.
US2003199010-A1.
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(GETH ) GEN
                                                                                                                                                                                                                                                         US2003207349-A1.
                                                                                                                                                                                                                                                                   ADI18326 standard; protein; 260 AA. Novel human secreted and transmembr
                                                                                                                                                                                                                                                                                                                                                       ADI14731 standard; protein; 260 AA.

Novel human secreted and transmembrane
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                                                       (GETH )
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane
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Novel human secreted and tra
US2004009548-A1.
15-JAN-2004.
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                                 Local Similarity
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standard; protein;
polypeptide #198.
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Best Loca
RESULT 364
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Best Local S
RESULT 361
ID ADM17394
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RESULT 363
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Best Local S
RESULT 359
   Query Match
Best Local Similarity
RESULT 358
ID ADK82850 standard;
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RESULT 362
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26-FEB-2004.
(GETH ) GENENTEC
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US2004058424-Al.
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                                                                                                                                         Human NOV11h.
US2004038223-A1.
26-FEB-2004.
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US2004048332-A1.
11-MAR-2004.
(GETH ) GENENTECH INC.
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Human PRO polypeptide #198.
US2004038335-A1.
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Human PRO polypeptide #36.
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(GETH ) GENENTECH
                                                                                             (XEXO)
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(GETH ) GEN
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MILLET I.
PEYMAN J A.
KEKUDA R.
JU J.
LI L.
GUO X.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
ORT T.
GORMAN L.
ZERHUSEN B D.
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Pred. No. 1.:
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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                                                                                                                                                                                        1.1e-40;
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Query Match
Best Local S
RESULT 371
ID AAB37985
DE Human sec
PN WO2000553
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Best Local Similarity
RESULT 368
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Best Local Similarity
RESULT 367
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                                                                                                Best Local Similarity RESULT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 365
ID ADN04214 standard;
                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                      Human PRO polypeptide #198. US2004077064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Antipsoriatic protein sequence #302 W02004028479-A2.
                                                                                                                                                                                                                                                                                Human PRO polypeptide #198. US2003077659-A1.
                                                                                                                                                                                                        Novel human secreted US2003207354-A1. 06-NOV-2003.
Human secreted WO200055371-A1.
       AAB37985 standard; protein; 306
Human secreted protein encoded l
                                                     (SUNR ) SUNTORY LTD.
                                                             24-AUG-1999
                                                                      JP11225765-A.
                                                                             AAY32853 standard; protein; 305 AA.
Human serine protease protein sequence.
                                                                                                        (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 45.9%;
t Local Similarity 50.2%;
                                                                                                                                   WO2004075713-A2.
10-SEP-2004.
                                                                                                                                                    Human ovarian
                                                                                                                                                             ADR72883 standard;
                                                                                                                                                                                                                                  ADI96380 standard;
                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.

"RY Match 45.

"L Local Similarity 50.
                                                                                                                                                                                                                                                                                                                                          22-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                GETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROTH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHEN/
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) RIEGER D K.
) SPADERNA S K.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
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BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STONE D J.
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50.2%;
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and transmembrane
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No. 1.1e-40;
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No. 1.1e-40;
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                                                                                                                                                      marker kallikrein
                                                                                                         ).5; DB 8;
1.1e-40;
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          N
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                                   DB 2;
          clone
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                                             305;
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Query Match
Best Local Similarity
RESULT 378

ID ABB57219 standard; p
DE Mouse ischaemic cond
PN W0200188188 A2:
PD 22-NOV-2001.
                                                                                                                                       Query Match
Best Local S
RESULT 379
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Best Local Similarity
RESULT 372
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Human ovarian antigen H
WC200200677-A1
03-JAN-2002
(HUMA-) HUMAN GENOME SC
Mouse neuropsin US6642013-B1. 04-NOV-2003.
                                ADI39731 standard;
                                                                                                    Murine NOVX protein W0200268649-A2.
                                                                                                                                                                                                                                                                                      AAY06438 standard; protein;
Human protease HUPM-7.
WO9936550-A2.
                                                                                                                          ADI17073 standard;
                                                                                                                                            (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

xy Match
45.3%; Score 622.5; DB 5
Local Similarity 49.0%; Pred. No. 4.5e-40;
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(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO
117 Match
45.3%; Score 62
11 Toral Similarity 49.0%; Pred. No
                                                                                                                                                                                                                                                              22-JUL-1999.
(INCY-) INCYTE PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A human serine protease designated EP887414-A2.
                                                                                                                                                                                                                                                                                                                                                                              Mouse neuropsin protein.
JP08311099-A.
                                                                                                                                                                                                                                                                                                                                                                                                   AAW12393 standard; protein; 260 AA
                                                                             CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP08245700-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB21311 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW10694 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neuropsin.
WO200053776-A2.
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ry Match
45.6%; Score
t Local Similarity 50.4%; Pred.
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ry Match 45.6%;
t Local Similarity 50.9%;
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                                                       Local Similarity
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                    protein.
                                                                                                                                                                                                       rd; protein; condition re
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                               protein;
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gen HCOQP78, s
                                                                                                            homologue
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45.6%; ;
50.4%; ;
                                                      45.3%;
49.0%;
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49.0%;
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45.6%;
50.9%;
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related protein
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ue SeqID
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Pred.
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No.
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No. 4.5e-40;
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No. 4.5
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No. 4.5e-40;
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No. 2.
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No. 2.2e-40;
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No. 2.4e-40;
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                                                    4.5e-40;
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4.5e-40;
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.4e-40;
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Best Local Similarity
RESULT 386
ID AAU12424 standard; p
DE Human PRO1279 polype;
PN W0200140466-A2.
PD 07-JUN-2001.
RESULT
ID AB
DE Pr
PN WC
PN WC
PD 18
PA (E
                                                                                    RESULT 388
ID AAU836
DE Human
PN WO2002
PD 31-JAN
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RESULT 384
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RESULT 383
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Best Local Similarity
RESULT 381
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Best Local :
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Best Local
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                ABG61816 standard; protein; Prostate cancer-associated; WO200230268-A2.
                                                                                                                                                     ABB50479 standard; protein; 250
Human secreted protein encoded t
WO200162891-A2.
30-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                              Human PRO protein, WO200208288-A2.
                                                                                                                 AAU83684 standard;
                                                                                                                                                                                                                                                        AAU12424 standard; protein; 250 AA Human PRO1279 polypeptide sequence. W0200140466-A2.
                                                                                                                                                                                                                                                                                                                            AAB66139 standard; protein; 2
Protein of the invention #51.
WO200079861-A1.
28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAY99390 standard; protein;
Human PRO1279 (UNQ649) amino
WO200012708-A2.
                                                                                     31-JAN-2002
                                                                            (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-2000
        8-APR-
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TY Match 45.0%;
t Local Similarity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TLSP.
                                                                                                                                                                                                                                                                                                                    (GETH )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB21325 standard;
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(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat NOVX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse neuropsin.
US2003199010-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI17074 standard;
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                                                                                                                                   local Similarity
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homologue
                                                                                                                                                                                                                                                                                                                  INC.
                                                                                                      protein; 250 AA.
Seq ID No 186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                   SCI INC.
45.0%;
48.2%;
                                                      45.0%;
48.2%;
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48.2%;
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48.2%;
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                         protein
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SeqID
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Pred. No.
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No.
                           #17
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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No.
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No.
                                                                                                                                   8.5; DB 4;
8.7e-40;
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8.7e~40;
                                                                                                                                                                                    179
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. 4.5e-40;
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BIOTECHNOLOGY

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RESULT 394
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US200304311-A1.
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W0200200690-A2.
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Human PRO polypeptide #93.
US2003036635-A1.
20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                           ABO33797 standard; protein; 250 AA. Novel human secreted and transmembrane US2003045687-A1.
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Novel human secreted and tra
                                                                              Lung cancer-associated WO200286443-A2.
                                                                                                 ABU56739 standard; protein; 250 AA Lung cancer-associated polypeptide
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Human angiogenesis related protein PRO1279
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(GETH ) GENENTECH
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
EOS BIOTECHNOLOGY INC.
h 45.0%; Score
Similarity 48.2%; Pred.
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  618.5; DB 6;
No. 8.7e-40;
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                                                                                                                                                              618.5; DB 6;
No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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8.7e-40;
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                       Human PRO polypeptide #253.
US2003054517-A1.
20-MAR-2003.
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US200336180-A1.
20-FEB-2003.
                                                                                                                                                                                 ADA76456 standard; protein;
Human PRO polypeptide #253.
US2003073212-A1.
17-APR-2003.
                                                                                                               ABJ72320 standard; protein;
Human PRO1279 protein.
US2003050448-A1.
                                                                                                                                                                                                                                                              Novel human secretus2003022328-A1. 30-JAN-2003.
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Novel secreted and
US2003017563-A1.
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Novel human secreted and tra
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Human secreted/transmembrane, PRO,
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US2003088063-A1.
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No. 8.7e-40;
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8.7e-40;
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Best Local Similarity
RESULT 414
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RESULT 408
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                                              Human PRO polypeptide #253. US2003068795-A1. 10-APR-2003.
  ADB30686
                                                                                                                                       ABO33632 standard; protein; 250 AA.
Novel human secreted and transmembrane
US2003073130-A1.
                                                                                                                                                                                                        Novel human secreted protein #179. US2003065160-A1. 03-APR-2003.
                                                                                                                                                                                                                                                                                                         ADA47884 standard; protein; Human PRO polypeptide #253.
                                                                                                                                                                                                                                                                                                                                                                             ADB16098 standard; protein;
Human PRO polypeptide #253.
US2003087350-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA86534 standard; protein; 250 AA.

Novel human secreted and transmembrane
US200308271.-A1.

(GETH) GENERVIECH INC.
                                                                                                                       17-APR-2003
(GETH ) GEN
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Human PRO polypeptide #253.
US2003082704-Al.
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US2003049816-A1.
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Novel human secreted and transmembrane
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48.2%; 1
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Pred. No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7
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No. 8.7e-40;
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8.7e-40;
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Best Local Similarity
RESULT 422
ID ADB14994 standard; p
DE Human PRO polypeptid
PN US2003087351-A1.
PD 08-MAY-2003.
                                                                                                                                                                                                                       Best Local Similarity
RESULT 421
ID ADA91931 standard; p
DE Novel human secreted
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH IN
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RESULT 420
ID ADB16839 standard; p
DE Human PRO polypeptid
PN US2003087349-A1.
PD 08-MAY-2003.
                    Best Local Similarity
RESULT 424
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Best Local Similarity
RESULT 419
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  Human
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Human PRO polypeptide #253.
US2003087351-A1.
                                                                               ADB18955 standard; protein; 250 AA.
Novel human secreted and transmembrane
                                                                                                                                                                                                                                          ADA91931 standard; protein; 250 AA. Novel human secreted and transmembrane US2003082694-A1.
           ADA94170 standard;
                                                                       US2003073211-A1.
                                                                                                                                       08-MAY-2003
(GETH ) GEN
                                                                                                                                                                                                                                                                                                                   ADB16839 standard; protein;
Human PRO polypeptide #253.
US2003087349-A1.
08-MAY-2003.
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US2003082693-A1,
01-MAV->^^
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Human PRO polypeptide #253.
US2003082705-A1.
01-MAY-2003.
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polypeptide #253.
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(GETH )
Query Match
Best Local f
RESULT 427
ID ABC43
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DE Human PRO polypeptide #253.
PN US2003082701-Al.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; S
Best Local Similarity 48.2%; P
RESULT 431
ID ADA75352 standard; protein; 25
Human PRO polypeptide #253.
PN US2003073216-Al.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.0%; EBBET Local Similarity 48.2%; IRESULT 428
ID ADA74632 standard; protein; 25
DE Human PRO polypeptide #253.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
                                                                                            Query Match
Best Local Similarity 4
RESULT 432
ID ADA85430 standard; pro
DE Novel human secreted a
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity
RESULT 433
ID ADA84878 standard; p
DE Novel human secreted
PN US2003082708-A1.
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RESULT 425
ID ADB20066 standard; pro
DE Novel human secreted a
PN US2003082691-A1.
PD 01-MAY-2003.
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Best Local S
RESULT 429
ID ADB24865 I
DE Human PRO
PN US2003077
PD 24-APR-20
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Best Local Similarity 48.2%;
RESULT 430
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Best Local Similarity 48.2%;
RESULT 426
                                                                                          ADA85430 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082695-A1.
01-MAY-2003.
(GETH) GENENTECH INC.
 ADA84878 standard; protein; 250 AA.

Novel human secreted and transmembrane protein PRO1279.
US2003082708-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB24865 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506. US2003077713-A1. 24-APR-2003.
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Human PRO polypeptide #253.
US2003068798-A1.
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Novel human secreted and transmembrane protein PRO1279.

US2003044945-A1.

06-MAR-2003.

(GETH) GENENTECH INC.
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Human PRO polypeptide #253.
US2003082710-A1.
01-MAY-2003.
(GETH) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1279.
US2003082691-A1.
01-MAY-2003.
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24-APR-2003.
(GETH ) GENENTECH INC.
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Local Similarity 48.2%;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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1 441 ROBERT PRO POLYPEPTIDE #2 US2003096386-A1. US2003096386-A1. (GETH) GENENTECH INC. TY MATCH T 442 R 142 R 143 R 144 R 1	244-APR-2003. (GETH) GENENTECH INC. TY MATCH LOCAL Similarity 48. T 1440 AD 26951 standard; prote ADB26951 standard; prote Human PRO polypeptide #2 US2003092147-A1. US2003092147-A1. Ty Match Local Similarity 48.	ADB25425 standard; prote Human PRO polypeptide SE US2003077715-A1. 24-APR-2003. (GETH) GENENTECH INC. Query Match Best Local Similarity 48. SULT 439 ADA93601 standard; prote Human PRO polypeptide #2 US2003077721-A1.	OSZOGJUSZ//J-AL. O1-MAY-2003. (GETH) GENENTECH INC. Duery Match 45. Best Local Similarity 48. SULT 437 ADA47129 standard; prote Human PRO polypeptide #2 US2003073210-A1. 17-APR-2003. (GETH) GENENTECH INC. Duery Match 1917 438 8117 438	ADA80662 standard; prot Human PRO polypeptide # US2003082761-A1. 01-MAY-2003. (GETH) GENENTECH INC. ery Match st Local Similarity 48 st Local Similarity 48 st Local Similarity 48 Human PRO polypeptide #	01-MAY-2003. (GETH) GENENTECH INC. Query Match Best Local Similarity 48. SULT 434 ADB30134 standard; prote Human PRO polypeptide #2 US2003073214-A1. 17-APR-2003. (GETH) GENENTECH INC. Query Match 25. Best Local Similarity 48. SULT 435
in; 250 AA. 53. 0%; Score 618.5; DB 6; 2%; Pred. No. 8.7e-40; in; 250 AA.	0%; Score 618.5; DB 6; 2%; Pred. No. 8.7e-40; in; 250 AA. 53. 53. 53. Score 618.5; DB 6; 2%; Pred. No. 8.7e-40;	in; 250 AA. Q ID NO 506. 0%; Score 618.5; DB 6; 2%; Pred. No. 8.7e-40; in; 250 AA.	0%; Score 618.5; DB 6; 2%; Pred. No. 8.7e-40; in; 250 AA. 53. 53. 53. Score 618.5; DB 6; 0%; Score 618.5; DB 6; 2%; Pred. No. 8.7e-40;	in; 250 AA. 53. 0%; Score 618.5; DB 6; L 2%; Pred. No. 8.7e-40; in; 250 AA. 53.	0%; Score 618.5; DB 6; 2%; Pred. No. 8.7e-40; in; 250 AA. 53. 53. 6%; Score 618.5; DB 6; 2%; Pred. No. 8.7e-40;
Length 250;	Length 250; Length 250;	Length 250;	Length 250;	ength 250;	Length 250; Length 250;

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Best Local Similarity
RESULT 451
ID ADA77663 standard; p
DE Human PRO polypeptid
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH IN
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RESULT 444
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RESULT 443
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                                                                                         ABO34343 standard; protein; 
Human secreted/transmembrane
US2003044934-A1.
                                                                                                                                                                                                                                      Human PRO polypeptide #253.
US2003082760-A1.
01-MAY-2003
                                                                                   06-MAR-2003
                                                                                                                                                                   Novel human secretus2003082765-A1.
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                                                                                                                                                                                      ADB21884 standard;
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                                                                                                                                                                                                                                                                                                             ADA96090 standard; protein;
Human PRO polypeptide #253.
US2003082759-A1.
01-MAY-2003.
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US2003082702-Al
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US2003049817-A1.
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DE Novel human secreted
PN US2003054516-A1.
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PA (GETH) GENENTECH INC
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                                                                                   Human protein from novel secreted p
US6525174-B1.
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Novel human secreted and tra
US2003082700-A1.
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06-MAR-2003.
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Human PRO polypeptide SEQ ID
US2003077712-A1.
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Human PRO polypeptide #253.
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Human membrane bound receptor/protein
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Human PRO polypeptide #253.
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Novel human secreted
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RESULT 473
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US2003088068-A1.
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US2003087352-Al.
08-MAY-2003
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                                                       Novel human secr
US2003082689-A1.
01-MAY-2003.
                                                                                                                                                                                                                         Novel human secreted and tra
                                                                                                                                          ADB39246 standard; protein; 250 AA.

Novel human secreted and transmembrane protein
US2003087347-A1.
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15-MAY-2003.
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                                                                          ADB66718 standard; protein; Novel human secreted and tra
                                                                                                                                 08-MAY-2003
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01-MAY-2003.
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US2003096968-A1.
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          ADB85053 standard;
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standard; protein; polypeptide #93.
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No. 8.7e-40;
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8.7e-40;
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01-MAY-2003.

(GETH) GENENTECH INC.

(GETH) 45.0%; §

Match 130rity 48.2%;
ADB83922 standard; protein; 250 AA. Novel human secreted and transmembrane US2003069397-A1.
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US2003082687-Al.
01-MAY-2009
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W0200210225-A2.
27-DEC-2002
(EOSB-) EOS BIOTECHNOLOGY INC.
(EOSB-) EOS BIOTECHNOLOGY FOR 45.0%; Score
48.2%; Pred.
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Human PRO polypeptide #93.
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US2003088067-A1.
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Human PRO polypeptide #93.
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Novel human secreted and tra
                                                                                                                                                                                                                                                                                                                           ADB78159 standard;
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US2003082762-A1.
01-MAY-2003
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Human PRO polypeptide SEQ ID US2003077720-A1.
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06-FEB-2003

(MILL-) MILLENNIUM PHARM INC.

(MILL-) 45.0%;

45.0%;

48.2%;
                                                                 24-APR-2003.
(GETH ) GENENTECH
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                                                                                                                                                          ADB34071 standard; protein; 250 Human PRO polypeptide SEQ ID NO US2003077716-A1.
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15-MAY-2003.
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Novel human secreted and transmembrane
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Pred. No. 8.7e-40;
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Query Match
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RESULT 506
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Human PRO polypeptide #51.
US2003064925-A1.
03-APR-2003.
                                                                                                                                                                                                  ADC60073 standard; protein; 250 AA. Novel human secreted and transmembrane US2003092105-A1.
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US2003092106-Al.
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Human PRO polypeptide #93.
US2003096969-A1.
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Human PRO polypeptide #93.
US2003088065-A1.
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Novel human secret
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US2003088064-A1.
                                                                                                                      ADC49936 standard; protein; 250 AA. Novel human secreted and transmembrane
                                                                                                                                                                                                                                                                                                      ADC72094 standard; protein; 250 AA. Novel human secreted and transmembrane
                                ADC49135 standard;
Novel human secret
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RESULT 525

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Best Local Similarity
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ID ADC48631 standard; p
DE Human PRO polypeptid
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PD 16-OCT-2003.
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RESULT 524
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RESULT 518
ID ADC58657 standard; F
DE Novel human secreted
PN US2003087346-A1.
PD 08-MAY-2003.
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Best Local Similarity
RESULT 532
ID ADC77887 standard; p
DE Novel human secreted
PN US2003088066-A1.
PD 08-MAY-2003.
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RESULT 533
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RESULT 531
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Best Local Similarity
RESULT 530
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RESULT 527
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                                        US2003087358-A1.
                                                ADC80139 standard; protein; 250 AA. Novel human secreted and transmembrane
                                                                                                                                                                                                                                                                    ADDI0497 standard; protein; 2
Human secreted/transmembrane
US2003105011-A1.
05-JUN-2003.
                                 08-MAY-2003
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Human PRO polypeptide #253.
US2003194771-A1.
16-OCT-2003.
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RESULT

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RESULT 535
ID ADD09608
DE Human PRO
PN US2003194
PD 16-OCT-20
Best I
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RESULT 542
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RESULT 538
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                                                 ADD53200 standard; protein;
Human PRO polypeptide #253.
US2003194792-A1.
16-OCT-2003.
                                                                                                                                                Human secreted/transmembrane US2003083462-A1.
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US2003194769-A1.
16-OCT-----
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US2003105290-A1.
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 ADD53752 standard;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Human PRO polypeptide #253.
US2003203430-A1.
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Human secreted/transmembrane
US2003096954-A1.
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22-MAY-2003.
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Human PRO polypeptide #93.
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22-MAY-2003.
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Human secreted/transmembrane
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30-OCT-2003.
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No. 8.7e-40;
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ADE20072 standard; protein; : Human secreted/transmembrane US2003092883-A1.
                                                       23-OCT-2003
(GETH ) GENENTECH
                                                                          ADE04150 standard; protein;
Human PRO polypeptide #253.
US2003199057-A1.
                                                                                                                                           Human PRO polypeptide #253. US2003199055-A1. 23-OCT-2003.
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US2003199030-A1.
23-OCT-2003
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US2003105289-A1.
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Human secreted/transmembrane
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Human secreted/transmembrane
US2003092061-A1.
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US2003096970-A1.
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No.
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8.7e-40;
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8.7e-40;
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8.7e-40;
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. 8.7e-40;
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Query Match
Best Local Similarity
RESULT 579
ID ADD79049 standard; pr
DE Human PRO polypeptide
PN US2003203429-A1.
PD 30-CCT-2003.
PA (GETH ) GENENTECH INC
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RESULT 575
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RESULT 576
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RESULT 574
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US2003199059-A1.
23-OCT-2002
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US2003199026-A1.
       Human PRO polypeptide #253.
US2003203429-A1.
                                                                                                                 ADE22931 standard; protein;
Human PRO polypeptide #253.
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Human PRO polypeptide #253.
US2003199033-A1.
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(GETH ) GENENTECH INC.
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Human secreted/transmembrane
US2003082628-A1.
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Human PRO polypeptide #253.
US2003194768-A1.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #253.
US2003199025-A1.
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Human secreted/transmembrane
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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RESULT 581

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US2003199034-A1.
23-OCT-2003.
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                           ADF55859 standard; protein; Human secreted/transmembrane US2003204054-A1.
                                                                                              ADF29966 standard; protein; ;
Human secreted/transmembrane
US2003204053-A1.
30-OCT-2003.
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Human FRO polypeptide #253.
US2003199031-Al.
23-OCT-2003.
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Human PRO polypeptide #253.
US2003207418-A1.
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US2003199032-A1.
23-Orm------
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Human PRO polypeptide #253.
US2003199028-A1.
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US2003194766-A1.
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PN US2003
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                                      Novel human secreted US2003207385-A1.
                                                                                                          ADH99363 standard; protein; ;
Human secreted/transmembrane
US2003065142-A1.
03-APR-2003.
                                                          ADI64207 standard;
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                    (GETH ) GENENTECH INC.
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(GETH ) GEN
                                                                                                                                                                                                                                                                       US2003207381-A1.
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NOVel human secreted and transmembrane
                                                                                               (GETH ) GENENTECH
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US2003207373-A1.
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US2001207277
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Pred. No. 8.7e-40;
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DE Novel
PN US2003
PD 08-MAY
PA (GETH
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RESULT 603
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RESULT 602
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08-MAY-2003.
(GETH ) GENENTERU ----
                              Novel human secr
US2003087357-A1.
08-MAY-2003.
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08-MAY-2003.
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Novel human secreted and tra
US2003087353-A1.
08-MAY-2003.
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08-MAY-2003.
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Novel human secreted and transmembrane
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Query Match
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RESULT 613
ID ADD75133
Query Match
Best Local S
RESULT 616
ID ADD86937
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RESULT 611
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RESULT 615
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15-MAY-2003.
(GETH) GENENTECH INC.
                                                                                                                                                                                                                  ADD75133 standard; protein;
Human PRO polypeptide #93.
US2003100712-A1.
29-MAY-2003.
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US2003100735-A1.
29-MAY-2007
                                                           ADD85111 standard; protein; 250 AA. Novel human secreted and transmembrane US2003100722-A1.
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US2003092115-Al
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(GETH ) GENENTECH
ADD86937 standard; protein;
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US2003207387-A1.
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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US2003203440-A1.
30-OCT-2007
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Human PRO polypeptide #93.
US200310071
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Human PRO polypeptide #253.
US2003092113-A1.
15-MAY-2003.
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                                                                 Novel human secr
US2003100737-A1.
29-MAY-2003.
                                                                                      ADD78483 standard; protein; 250 AA. Novel human secreted and transmembrane
                                                                                                                                                            ADE75907 standard; protein;
Human PRO polypeptide #253.
US2003211571-A1.
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29-MAY-2003.
     ADE41458 standard; protein; 2
Human secreted/transmembrane
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US2003100497-A1

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ADD85617 standard; protein; 250 AA Novel human secreted and transmemb; US2003100721-A1.
                                                                     US2003100718-A1.
29-MAY-2003.
                                                                                     ADD76125 standard; protein; 250 AA.
Novel human secreted and transmembrane
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15-MAY-2003.
(GETH) GENENTECH INC.
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US2003100736-A1.
29-MAY-2003.
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                                                           (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #93.
US2003100064-A1.
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Novel human secreted and tra
US2003100732-Al.
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29-MAY-2003.
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Human PRO polypeptide #253.
US2003092108-A1.
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Query Match
Best Local Similarity
RESULT 643
ID ADD78159 standard; p
DE Novel human secreted
PN US2003100731-A1.
PD 29-MAY-2003.
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RESULT 641
ID ADD86691 standard; p
DE Novel human secreted
PN US2003100719-A1.
PD 29-MAY-2003.
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RESULT 640
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ADD78159 standard; protein;
Novel human secreted and tra
US2003100731-A1.
29-MAY-2003.
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(GETH) GENENTECH INC.
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US2003100715-A1.
29-MAY-2003
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Human PRO polypeptide #253.
US2003199062-A1.
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(GETH ) GENI
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Human PRO polypeptide #93.
US2003100726-A1.
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Human PRO polypeptide
US2003092111-A1.
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ID ADD856
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PD 29-MAY
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US2003100713-A1.
29-MAY-2003
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US2003100710-A1.
29-MAY-200
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US2003100730-Al.
29-MAY-2003
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Human PRO polypeptide #253.
US2003199054-A1.
         US2003100720-A1.
29-MAY-2003.
                               ADD85863 standard; protein; Novel human secreted and tra
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #253.
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                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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Pred. No. 8.7e-40;
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No.
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No. 8.7e-40;
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US2003199052-A1.
23-OCT-2003.
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US2003199061-A1.
23-OCT-2003.
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                          ADF24753 standard; protein; ;
Human secreted/transmembrane
US2003198993-A1.
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Human secreted/transmembrane
US2003199675-A1.
23-OCT-2003.
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Human PRO polypeptide #253.
US2003199027-A1.
23-OCT-2003.
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No. 8.7e-40;
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Best Local Similarity
RESULT 670
ID ADG02422 standard; p
DE Human PRO polypeptid
PN US2003207352-A1.
PD 06-NOV-2003.
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RESULT
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RESULT 664
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                                   Human PRO polypeptide #253. US2003207352-A1.
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Novel human secreted and transmembrane
US2003096959-A1.
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Novel human secreted and transmembrane
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US2003199029-A1.
23-OCT-2003.
ICGETH) GENENTECH INC.
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  Local Similarity
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669
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No. 8.7e-40;
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8.7e-40;
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Best Local Similarity
RESULT 677
ID ADF99307 standard; p:
DE Human PRO polypeptide
PN US2003207353-A1.
PD 06-NOV-2003
PA (GETH ) GENENTECH INC
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RESULT 676
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RESULT 675
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RESULT 672
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ID ADG22208 standard;
DE Novel human secrete
PN US2003207360-A1.
                 Query Match
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US2003207353-A1.
06-NOV-2003.
                                       Human PRO polypeptide #253. US2003207375-A1.
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US2003207359-A1.
06-NOV-2007
                                     US2003207375
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Human PRO polypeptide #253.
US2003207351-A1.
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                             (GETH )
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Novel human secreted and transmembrane
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Human PRO polypeptide #253.
US2003207376-A1.
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U32003207425-A1.
06-NOV-2003.
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                                                                                                                                     ADG06265 standard; protein;
Human PRO polypeptide #253.
US2003207374-A1.
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Human PRO polypeptide #253.
US2003207371-A1.
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US2003207357-A1.
06-NOV-2000
                                                        ADG23849 standard; protein; 250 AA. Novel human secreted and transmembrane US2003207389-A1.
ADG04138 standard; protein;
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22-MAY-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity RESULT 698
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US2003207427-Al.
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US2003207350-A1.
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06-NOV-2003.
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16-OCT-2003.
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Novel human secreted and transmembrane
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ADH03058 standard; protein; 2
Human secreted/transmembrane
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protein PRO1279

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ADH39092 standard;
Novel human secret
US2003096965-A1.
                                                                                  ADH03535 standard; protein; 2
Human secreted/transmembrane
US2003224478-A1.
                                                                         04-DEC-2003
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27-NOV-2003.
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1279.

US2003207365-A1.
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Novel human secreted and transmembrane
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20-NOV-2003.
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Novel human secreted and transmembrane
US2003207416-A1.
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(GETH ) GENENTECH INC.
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Novel human secreted and tra
US2003207367-A1.
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                                    ADH04489 standard; protein; ;
Human secreted/transmembrane
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                                    ADI29907 standard; protein; Novel human secreted and traUS2003096961-A1.
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                                              in; 250 AA.
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No. 8.7e-40;
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8.7e-40;
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Best Local Similarity
RESULT 742
ID ADM27870 standard; p
DE Human PRO polypeptid
PN US200404833-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH IN
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RESULT 738
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RESULT 736
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                             ADM42594 standard; protein;
Human PRO polypeptide #253.
US2004058424-A1.
25-MAR-2004.
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26-FEB-2004.
(GETH ) GENENTECH INC.
45.0'
Match 45.0'
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04-MAR-2004.
                                                                                                                                                                               ADJ65734 standard; protein;
Human PRO polypeptide #253.
US2004038335-A1.
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US2004043927-A1.
04-MAR-2004
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US2004038336-A1.
26-FEB-2004
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Novel human secreted and tra
US2004039164-Al.
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No. 8.7e-40;
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No. 8.7e-40;
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RESULT 753
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RESULT 751
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                                                              Human serine
                                                                                                                         CASB12 amino acid
WO9949055-A1.
                                                     WO200031257-A1.
                                                                                                                                                                                              ADS34892 standard; protein; 250 / Human autoimmune disease-related W02004083403-A2.
                                                                                                                                                                                                                                                             Human ovarian cancer-related W02004075713-A2.
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10-SEP-2004.

(MOUN ) MOUNT SINAI HOSPITAL.

45.0%;

27 March
48.2%;
                                     (FUSO)
                                                                     AAB11712 standard;
                                                                                                                                           AAY42439 standard;
                                                                                                           (SMIK)
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ry Match 45.0%;
t Local Similarity 48.2%;
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Human renal cell c
                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secretus2003207354-A1.
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Human PRO polypeptide #253.
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Human secreted/transmembrane
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                                   FUSO
                 Similarity
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 standard;
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protease BSSP6
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(hBSSP6)
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d tumour marker
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RESULT 756
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                                                                                 AAB67542 standard; protein; 288 AA. Amino acid sequence of catalytic domain
                                                                                                                                                        Fusion gene with WO200066709-A2.
                                                                                                                                                                                                                                                AAY42440 standard;
CASB12 polypeptide
                                                                                                              (ORTH ) ORTHO-MCNEIL PHARM | 43.9%; t Local Similarity 51.1%;
                                                                                                                                                                AAB36482 standard; protein; 288 AA.
Fusion gene with human serine prote
                                                                                                                                                                                                                                                                                                                                  Human autoimmune
                                                                                                                                                                                              (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
ry Match 44.6%; Score 612.
Local Similarity 48.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                      WO2004083403-A2.
                                                                                                                                                                                                                                                                                                                                          ADS34893 standard; protein; 282 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR72631 standard; protein;
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Human kallikrein-11, marker
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                                                                                                                                                                                                                                                                                                  (APPL-) APPLERA CORP.
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ry Match 45.0%;
t Local Similarity 48.2%;
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  3 standard;
1 human secr
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                                                     ORTHO-MCNEIL PHARM INC.
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ard; protein; 250 secreted protein
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No.
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No.
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No. 9.9
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No. 9.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kallikrein
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No.
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                                                                                                               .5; DB 3;
1.7e-38;
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9.9e-40;
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9.9e-40;
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1.7e-38;
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.8e-39;
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.9e-40;
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RESULT 765
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Best Local Similarity
RESULT 763
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Best Local (
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AAB67543 standard; protein; 289 Amino acid sequence of catalytic WO200116289-A2.
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                                                                                                                                                                                                                                                                                                                        Murine NOVX protein WO200268649-A2.
                                                                                        AAB36483 standard; protein; 289 AA. Fusion gene with human serine protease
                                                                                                                                                            Human kallikrein
WO2004029285-A2.
                                                                                                                                                                                                                                          WO200214485-A2.
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ry Match 43.6%;
t Local Similarity 46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                     Human protease, WO200208396-A2.
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xry Match 43.7%;
t Local Similarity 44.2%;
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Human secreted poli
US2004110939-A1.
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Human protease, PRTS-3 protein.
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115, marker
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e of novel
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43.6%;
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47.1%;
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c domain
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3.3e-38;
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1.8e-38;
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.8e-38;
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.8e-38;
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            PFEK1-6XHIS-TAG
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RESULT 772
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Human KLK-L6 protein #2.
W0200053776-A2.
                                                                          Pig pro-trypsin.
US2004043455-A1.
                                                                                                                                                        ABB98258 standard; protein;
Pig trypsinogen SEQ ID NO 1.
WC200261064-A2.
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Human PS133 consensu
US6232456-B1.
15-MAY-2001.
(ABBO) ABBOTT LAB.
                                                                                            ADJ92132 standard;
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Human TLSP.
WO200053776-A2.
                                                                                                            (HOFF) ROCHE DIAGNOSTICS GMBH.
(HOFF) HOFFMANN LA ROCHE & CO AG

TY MATCH
Local Similarity 45.6%; Pred.
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(NOVO ) NOVO-NORDISK AS.
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                                                                                                                                                                                                                                           Porcine trypsinogen.
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Human NOVX protein
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06-SEP-2002.
                                                                                                        Local Similarity
779
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h 43.5%;
Similarity 47.0%;
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                                    $ BIOTECH INC.
41.7%; S
2y 45.6%; P
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43.1%;
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45.6%;
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48.1%;
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47.8%;
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No. 2.
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No. 8.
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No. 2.8e-36;
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No.
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No. 3.
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                                      DB 8;
.8e-36;
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1.6e-38;
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Query
Best Loc
RESULT 789
ID ADL71'
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PN W'
PD
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RESULT 787
ID AAB21300 standard; p
DE Human KLK-L4 protein
PN W0200053776-A2.
PD 14-SEP-2000.
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RESULT 786
ID ADNOSSI6 standard, p
DE Antipsoriatic protei
PN W02004028479-A2.
PD 08-ARR-2004.
PA (GETH) GENENTECH IN
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RESULT 782
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Best Local Similarity
RESULT 781
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                                                                             Novel human polypeptide #141. W02003023013-A2. 20-MAR-2009
            Human kallikrein 13
WO2004021009-A2.
                           ADL71094 standard; protein;
                                                                                                                                                             Human KLK-L4 protein WO200053776-A2.
                                                                                                                                                                      AAB21300 standard; protein;
Human KLK-L4 protein #2.
                                                                                                                                            (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                       Antipsoriatic protein WO2004028479-A2.
                                                                                                                                                                                                                                                                                                        24-APR-2003
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                                                                                                                                                                                                                                                                                                                                   ABR55400 standard;
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Human protein SEQ 1
WO200259260-A2.
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Human KLK-L3 protein
WO200053776-A2.
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Human protein modif
WO2003000844-A2.
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Human kallikrein 14, marker
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                                                                 HYSEQ INC.
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9e-36;
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ID AAY384
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                                                                                                                                                                            AAY38412 standard; protein; 293 Human secreted protein encoded WO9935158-A1.
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                                                                                                         AAY38426 standard; protein; 293
Human secreted protein encoded |
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                    WO9963088-A2.
                            AAY66726 standard;
Membrane-bound prof
                                                                                              Human secreted WO9935158-A1.
                                                                                                                                                                                                                                                                             AAY30524 standard; protein;
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Novel human enzyme polypeptide
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e 564.5; DB 2;
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                              Human secreted p
WO2002102994-A2.
27-DEC-2002.
                                                                                                                            ABO17843 standard; protein; 293 AA.
Novel human secreted and transmembrane
US2003032156-A1.
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Novel human secreted or tran
US2002132252-A1.
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Human PRO polypeptide #96.
US2003027163-A1.
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WO200053776-A2.
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Human secreted protein #257.
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WO200109327-A2.
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Human PRO1132 (UNQ570) prote
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Human PRO1132 polypeptide sequence.
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Best Local Similarity
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  ADA41305
                                                       ADA41303 standard; protein;
Human secreted protein.
WO2002102993-A2.
                                                                                                                                 ABU66797 standard; protein;
Human PRO polypeptide #228.
US2003036180-A1.
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                                                                                                              (GETH ) GENENTECH INC
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Human secreted/transmembrane pro
US2002160384-A1.
31-OCT-2002.
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Human secreted protein #257,
WO2002102994-A2.
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WO2002102994-A2.
27-DEC-2000
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RESULT 826
ID ABU59438 standard; g
DE Novel human secreted
PN US2003027985-A1.
PD 06-FEB-2003.
                                                                          Query Match
Best Local Similarity
RESULT 825
ID ABU92373 standard; p
DE Novel human secreted
PN US2003022187-A1.
PD 30-JAN-2003.
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RESULT 823
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12-SEP-2002.
(GETH) GENENTECH INC.
(GETH) 41.1%;
Match 17-1ty 45.3%;
ABU59438 standard; protein; 293 AA. Novel human secreted or transmembrane US200307985-A1.
                                                                             Novel human secreted and transmembrane US2003022187-A1.
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Human secreted/transmembrane
US2003027162-A1.
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Novel secreted and
US2003017563-A1.
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27-DEC-2002.
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US2003073212-A1.
17-APR-2003
                         ADA19056 standard; protein;
Human PRO polypeptide #228.
US2003054517-Al.
20-MAR-2003.
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Human secreted and
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US2002123463-A1.
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Novel human secreted and tra
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28-NOV-2002.
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US2003087350-A1.
08-MAY-2003
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Human secreted/transmembrane
US2003054404-A1.
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Human PRO polypeptide #228.
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ADA67629 standard; protein;
Human PRO polypeptide #228.
US2003068795-A1.
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27-MAR-2003.
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Human secreted/transmembrane
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US2003082704-A1.
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13-MAR-2003.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #228.
US2003087349-A1.
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Novel human secreted and transmembrane protein
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Human secreted/transmembrane
US2003059832-A1.
                                                          ADB24815 standard;
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #228.
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US2003087351-A1.
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Novel human secreted and transmembrane
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RESULT 865
ID ADA75302 standard; protein; 29
EH Human PRO polypeptide #228.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENWERT ***
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RESULT 870
ID ADA75854 standard; protein; 29
DE Human PRO polypeptide #228.
PN US2003082703-A1.
PD 01-MAY-2003.
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RESULT 871
ID ADA38750 standard; p)
DE Human secreted/transs
PN US2033059780-A1.
PD 27-MAR-2003.
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(GETH ) GENENTECH INC.
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                                                                                    ADA47079 standard; protein;
Human PRO polypeptide #228.
US2003073210-A1.
                                                                                                                                                                          ADA38750 standard; protein; 293 AA. Human secreted/transmembrane protein US2003059780-A1.
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Human PRO polypeptide #228.
US2003073214-A1.
17-APR-2003.
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Novel human secreted and transmembrane protein PRO1132.
US2003082695-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
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Human PRO polypeptide #228.
US2003082701-A1.
ADB25375 standard; protein; 293 AA. Human PRO polypeptide SEQ ID NO 456
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ADA81164 standard; p Human PRO polypeptid US2003082702-A1. 01-MAY-2003. (GETH) GENENTECH IN ery Match ery Match ET Jocal Similarity ET B82 ADA96040 standard; p Human PRO polypeptid US2003082759-A1. 01-MAY-2003.	SULT 880 ADA96592 standard; p Human PRO polypeptid US2003082690-A1. 01-MAY-2003. (GETH) GENENTECH IN Query Match Query Match SULT 881	ADB24263 standard, p Human PRO polypeptid US2003077714-A1. 24-APR-2003. (GETH) GENENTECH IN Query Match Best Local Similarity	ADA61116 standard; p Homo sapiens. US2003049817-A1. 13-MAR-2003. (GETH) GENENTECH IN Query Match Query Match	ADA92871 standard; p Human secreted/trans US2003060407-A1. 27-MAR-2003. Query Match Query Match Similarity	ADB31188 standard; p Human PRO polypeptid US2003096386-A1. 22-MAY-2003. (GETH) GENENTECH IN Query Match Query Match	ADB26901 standard; p Human PRO polypeptid US2003092147-A1. 15-MAY-2003. (GETH) GENENTECH IN Query Match Query Match	ADA93551 standard; p Human PRO polypeptid US2003077721-A1. 24-APR-2003. (GETH) GENENTECH IN Query Match Query Match SULT 875	US2003077715-A1. 24-APR-2003. (GETH) GENENTECH IN Query Match Best Local Similarity
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US2003082706-A1
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Human PRO polypeptide #228.
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                              ADA39291 standard; protein;
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Human PRO polypeptide #228.
US2003022239-A1.
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Human PRO polypeptide #228.
US2003082686-A1.
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08-MAY-2007
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01-MAY-2007
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein
US2003082712-A1.
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Human PRO polypeptide SEQ ID NO 456.
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24-APR-2003.
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WO2002102235-A2.
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Human PRO polypeptide SEQ ID
US2003077717-A1.
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Human PRO polypeptide #228.
US2003082697-A1.
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Novel human secreted and transmembrane
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24-APR-2003.
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10-APR-2003.
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Human secreted/transmembrane
US2003049681-A1.
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US2003027754-Al.
06-FEB-2007
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Human PRO polypeptide SEQ II
US2003077716-A1.
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                         ADD08679 standard; protein; Novel human secreted and traus2003073090-A1.
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ADD56240 standard; protein;
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                                                    ADD55282 standard; protein;
Human PRO polypeptide #96.
US2003077593-A1.
                                                                                                                        ADD53702 standard; protein; 293 AA. Novel human secreted and transmemb; US2003203437-A1.
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Human PRO polypeptide #96.
US2003059783-A1.
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Human PRO polypeptide #228.
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Human PRO polypeptide #96.
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US2003199064-A1.
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PD 08-MAY-2003.
PA (GETH ) GENENTECH IN
Best Local Similarity 41.1%; Score 564.5; DB 7; Leng RESULT 1022

ID ADC81193 standard; protein; 293 AA.

DE Novel human secreted and transmembrane protein PRO1132. PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENERALT.
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Best Local Similarity
RESULT 1017
ID ADN16035 standard; pr
DE Novel human secreted
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC
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Best Local Similarity
RESULT 1014
ID ADH99982 standard; p
DE Novel human secreted
PN US2003049682-A1.
PD 13-MAR-2003.
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ID ADN1666
DE Novel h
PN US200301
PD 08-MAY-
PA (GETH)
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Novel human secreted and transmembrane protein PRO1132.
US2003087385-A1.
08-MAY-2003.
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Novel human secreted and transmembrane protein PRO1132
US2003087356-A1.
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Novel human secreted and transmembrane
US2003087353-A1.
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Novel human secreted and transmembrane protein PRO1132.
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                                                   ADE92345 standard; protein; 293 AA. Novel human secreted and transmembrane
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Human PRO polypeptide #228.
US2003199029-A1.
23-OCT-2003.
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Human PRO polypeptide #228.
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Human PRO polypeptide #228.
US2003199061-A1.
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Human PRO polypeptide #228.
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Novel human secreted and transmembrane
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Human PRO1132 polypeptide.
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RESULT 1054

ID ADG19568 standard; pr.
DE Human PRO polypeptide
PN US2003207425-1
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US2003207425-A1.
06-NOV-2007
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US2003207359-A1.
06-NOV-2007
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Human PRO polypeptide #228.
US2003207357-A1.
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US2003207353-A1.
06-NOV-2007
                                                                ADF97030 standard; protein;
Human PRO polypeptide #228.
US2003207371-A1.
                                                                                                                                                  ADG15632 standard; protein;
Human PRO polypeptide #228.
                                                                                                                                                                                                                             ADG08462 standard; protein; Novel human secreted and tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG05301 standard; protein;
Human PRO polypeptide #228.
US2003207375-A1.
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27-NOV-2003.
ADG06215 standard; protein;
Human PRO polypeptide #228.
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RESULT 1065
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06-NOV-2003.
(GETH) GENENTECH INC.
41.1%; (
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06-NOV-2003.
(GETH ) GENENTECH INC.
41.1%; (MARCH '17-YEY 45.3%;
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US2003207423-A1.
06-NOV-2003
                                                                                                  ADG62101 standard; protein; 293 AA. Novel human secreted and transmembrane
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06ETH ) GENENTECH INC.
(GETH ) 41.1%;
41.1%;
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         ADG82302 standard; protein;
Human PRO polypeptide #228.
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US2003207358-A1.
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Pred. No. 1.5e-35;
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ADG81750 standard; protein;
Human PRO polypeptide #228.
US2003207805-A1.
06-NOV-2003.
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06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secrete
US2003207363-A1.
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US2003207365-Al.
06-NOV-2003.
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                                             Local Similarity
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Novel human secreted and transmembrane
US2003207364-A1.
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06-NOV-2003.
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Query Match
Best Local Similarity
RESULT 1085
ID ADH12703 standard; p
DE Novel human secreted
PN US2003207378-A1.
PD 06-NOV-2003.
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ID ADM2077
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                                      ADH21048 standard; protein; ;
Human secreted/transmembrane
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Novel human secreted and transmembrane
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US2003194793-A1.
16-OCT-2007
                                US2003224358-A1.
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Novel human secreted and transmembr
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Human secreted/transmembrane
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Human PRO polypeptide #228.
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US2003022331-A1.
30-JAN-2007
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Novel human secreted and transmembrane
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Novel human secreted and transmembrane
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                            US2004009547-A1.
15-JAN-2004.
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Novel human secreted and transmembrane
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                                                   Amino acid sequence WO200200860-A2.
                                                                                                                                                    ABG96356 standard; protein; Human ovarian cancer marker
                                                                                AAU82729 standard;
                                                                                                                                            WO200271928-A2.
                                                                                                                                                                               (MOUN) MOUNT SINAI HOSPITAL.

ry Match 41.0%;
t Local Similarity 45.9%;
                                                                                                                                                                                                                          Human NES1.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                         AAW07620 standard; prot
Human NES1 polypeptide.
WO9639175-A1.
                                                                                                                                                                                                                                             AAB21327 standard;
                                       SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                 12-DEC-1996.
(NEWE-) NEW ENGLAND
                                                                                                                                                                                                                                                                                                                                                                                               AAY14072 standard; protein; 322
Human BS247 specific epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR72873 standard; protein; 2
Human ovarian cancer-related
WO2004075713-A2.
10-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                   (ABBO ) ABBOTT LAB.
               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOUN ) MOUNT SINAI HOSPITAL.

ry Match
t Local Similarity 45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI96440 standard; protein; 293 AA. Novel human secreted and transmembrane US2003207354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human renal cell WO2004077060-A2.
                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR72621 standard;
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Human PRO polypeptide #228.
US2003077659-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                       MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d; protein; 293 AA. carcinoma-related
                                                                   protein; 276 AA
e of novel human
protein;
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                                                                                                                                                                                                                                                                                                                            protein;
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41.0%;
45.9%;
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41.1%;
45.3%;
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45.9%;
                   45
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45.3%;
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45.3%;
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45.3%;
                    . 9%;
                                                                                                                                                    276 AA.
OV32.
 276 AA
                                                                                                                                                                                                                                              276
                                                                                                                                                                                                                                                               CENT HOSPITALS INC.
Score 564; DB 2;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                           276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AA.
                   Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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                   564;
No. 1.
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No. 1.
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No. 1
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No. 1.6
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No.
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No.
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No. 1.
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1.5e-35;
                  DB 5;
.5e-35;
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.5e-35;
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.5e-35;
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Query Match
Best Local Similarity
RESULT 1122
ID AAB21299 standard; p
DE Human KLK-L4 protein
PN W0200053776-A2.
PD 14-SEP-2000.
                    Best Local Similarity
RESULT 1123
                                                                                                                                                                                            Best Local Similarity
RESULT 1121
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RESULT 1119
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RESULT 1117
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RESULT 1116
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Best Local Similarity
RESULT 1115
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AAB21309 standard;
Human KLK-L2.
                                                                Human KLK-L4 protein #1.
W0200053776-A2.
14-SEP-2000
                                                                                                                                                       Human KLK-L6 protein #1.
W0200053776-A2.
                                                      (MOUN )
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(MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                          ADR72886 standard; protein; 2 Human ovarian cancer-related
                                                                                                                                                                                                                                                                                        (MOUN ) MOUNT SINAI HOSPITAL.

STY Match

tt Local Similarity 45.9%;
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Human renal cell ca
                                                                                                                                                                                                                                                                                                                                                                                                              ADQ89070 standard; protein; 276 AA. Human urological disorder related p W02004065576-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN04446 standard; protein; Antipsoriatic protein sequer W02004028479-A2.
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ry Match 41.0%;
t Local Similarity 45.9%;
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Human kallikrein 10
WO2003070883-A2.
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XY Match 41.0%; {

Local Similarity 45.9%; I
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                                                  MOUNT SINAI
                                                                                                                                       MOUNT SINAI
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h 41.0%; Score
Similarity 45.9%; Pred.
                                                                                                                                                                                                                                                                                                                                              d; protein; 276 AA carcinoma-related
         protein;
                            HOSPITAL.
40.9%;
49.1%;
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40.9%;
48.1%;
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0 (gene ID
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45.9%;
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D 2045)
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Pred.
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No.
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No. 1
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No. 1
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No. 1.5e-35;
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No. 1
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No. 1.5e-35;
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No. 1.5e-35;
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RESULT
ID AI
DE ON
PN WC
PD 27
PA (E
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ID AA
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PN JP
PD 10
                    RESULT 1132
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  BE
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RESULT 1125
ID AAB21310 standard;
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                                                                                                                         Query Match
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(ELIL ) LILLY & CO ELI.
(ELIL ) LILLY & CO #40.8%; f
                                                          Ovarian cancer-associated protein # W02002102235-A2.
                                                                                                                                                                 AAE37572 standard; protein;
Human 2047 protein.
                                                                                                                                                                                                                                        Human zyme.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                       AAW22985 standard; protein;
Human serine protease 59 (SI
JP09149790-A.
ADN39212 standard; protein; 244 AA. Cancer/angiogenesis/fibrosis-related
                                                                                                                                              WO2003037258-A2.
08-MAY-2003.
                                                                                                                                                                                                                                                             AAB21323 standard;
                                                                                                                                                                                                                                                                                                                                            AAW51006 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyme APP-cleaving protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR44532 standard; protein;
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14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOPF) ROCHE DIAGNOSTICS GMBH.
(HOPF) HOPFMANN LA ROCHE & CO AG
(HOPF) HOPFMANN 40.8%; Score
ry Match 40.7%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOUN ) MOUNT SINAI
                                                                                                                                                                                              MOUN ) MOUNT SINAI HOSPITAL.

TY Match 40.8%;
Local Similarity 46.7%;
                                                   EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                   MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                     DAND ) DANA FARBER
                                                                                                                                                                                                                                                                                                                                                                                      SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUN ) MOUNT SINAI
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40.9%;
46.1%;
                                                                                                                                                                                                                                                                               CANCER INST INC.
40.8%; Score 561;
46.7%; Pred. No. :
                                                                                                                                                                                                                                                                                                                                  serine protease
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trypsinogen SEQ
                                                                                                               40.8%;
46.7%;
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46.7%;
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46.7%;
                               40.8%;
46.7%;
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(SP59).
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Pred.
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No. 2.
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No. 2
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No. 2.3e-35;
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No. 2
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No.
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polypeptide,
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2.3e-35;
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2.5e-35;
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2.3e-35;
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2.3e-35;
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.3e-35;
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  NO:530
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Query Match
Best Local S
RESULT 1141
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Best Local S
RESULT 1138
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Best Local Similarity
RESULT 1140
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RESULT 1135
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20-MAY-2004.
(ISIS-) ISIS PHAR
                                                                                                                                                                   W0200053776-A2.
14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN04074 standard; protein; 244 AA. Antipsoriatic protein sequence #232. W02004028479-A2.
AAW05383 standard; protein;
Human amyloid precursor prot
WO9631122-A1.
                                                                                                      AAR67888 standard; protein; 253 AA.
Human stratum corneum chymotrophic
                                                                                                                                      (MOUN ) MOUNT SINAI HOSPITAL.

ry Match 40.5%;
t Local Similarity 46.1%;
                                                                                                                                                                                                                                                                                ABG96357 standard; protein; Human ovarian cancer marker WO200271928-A2.
                                                                                                                                                                                                                                                                                                                                                                         Human ovarian cancer-related WO2004075713-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR72624 standard; protein; 244 AA. Human renal cell carcinoma-related W02004077060-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ89076 standard; protein; 244 AJ
Human urological disorder related
                                                                    (SYMB-) SYMBICOM
                                                                                 05-JAN-1995.
                                                                                           WO9500651-A1.
                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                           (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 40.8%;
t Local Similarity 46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                   ADR72876 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 40.8%;
t Local Similarity 46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human urological
WO2004065576-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN29289 standard; protein; 244 AA.
Human kallikrein 6 associated prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-APR-2004.
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                                              Local Similarity
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46.7%;
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                                              40.4%;
44.6%;
          protein
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                                                                                                                                                                                                                                                                                            244 AA.
OV33.
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Pred.
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Pred. No. 2.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                       tumour
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Pred. No. 2.
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          protease
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                                              555;
No. 6.
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No. 2.
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No. 5.
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No. 2.
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No. 2
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No. 2.
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No. 2.3e-35;
                                                                                                       recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kallikrein
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;.7e-35;
                                              DB 2;
.9e-35;
                                                                                                                                                                                                                                                                                                                               DB 8;
.3e-35;
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.3e-35;
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.3e-35;
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.3e-35;
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                                                                                                                                                                                                                                                                                                                                                                                       kallikrein
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                                                                                                                                                                                                                                                                                                                                                                                       protein
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JS-A2
JO2.
JS-A2
J
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ID AD
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Best Local Similarity
RESULT 1145
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RESULT
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Best Local Similarity
RESULT 1143
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Best Local Similarity
RESULT 1142
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                                                                                               Human heat mitochondrial protein W02003087768-A2. 23-OCT-2003.
 ADN39180 standard;
                                                                                                                                                                                                                                                             ADB80484 standard; protein; 253 AA. Ovarian cancer-associated protein # W02002102235-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein differentially regulated in W0200281638-A2. 17-0CT-2002.
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Human SCCE protein |
WO200262135-A2.
15-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR58471 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU07440 standard; protein; Protein differentially regu
                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200281638-A2.
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15-AUG-2002.
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                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human SCCE protein
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(ELIL ) LILI
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(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EGEL/) EGELRUD (HANS/) HANSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                               EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGENE TECHNOLOGIES
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                                                                      AGE
 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 253 AA.
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40.4%;
44.6%;
                                 40.4%;
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N-terminal fragment
                                                                                                                                                                                                                                                                                                                                  40.48;
44.68;
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44.68;
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regulated in
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253 AA
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Pred.
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                               555;
No. 6.
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No. 6.
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No. 6.
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No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme
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No. 6.
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No. 6.9e-35;
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No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate cancer
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                                                                                                                                    therapeutic
                                                                                                                                                                                                                                                                                                                                  5; DB 6;
6.9e-35;
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                               DB 7;
.9e-35;
                                                                                                                                                                                          DB 7;
.9e-35;
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.9e-35;
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.9e-35;
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.9e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                        ovarian
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                                                                                                                                    target SeqID639
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                                                253;
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Best Local Similarity
RESULT 1155

ID ADN62898 standard; pl
DB Human NOVU8b.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (MILL) MILLET I.
PA (PEM) PEYMAN J A.
PA (MILL) HILLET I.
PA (PEM) KEKUDA R.
PA (LILL) LI L.
PA (GUOX) GUO X.
PA (JUJJ) JU J.
PA (SPIT) PATTURAJAN M
PA (SPIT) PATTURAJAN K.
PA (ELLE) ELLERMAN K.
PA (ELLE) ELLERMAN K.
PA (ELLE) ELLERMAN L.
PA (CORT) GORT T.
PA (GORM) GORMAN L.
PA (CATT) DATTERTON B. D
PA (ANDE) ANDERSON D W
PA (ZHON) ZHONG M.
PA (CATT) CATTERTON E.
PA (MILL) MILLER C E.
PA (MILL) MILLER C E.
PA (STON) STONE D J.
PA (STON) STONE D J.
PA (SHEM) SHENOY S G.
PA (BERG) BERGHS C.
PA (BERG) BERGHS C.
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Best Local S
RESULT 1151
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RESULT 1154
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RESULT 1152
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Human NOV18b protein
WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN04182 standard; protein; 253 AA. Antipsoriatic protein sequence #286. WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004075713-A2.
10-SEP-2004.
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Human ovarian cancer-related tumour marker kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL06515 standard; protein; Human tumour-associated ant:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR72880 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer/angiogenesis/fibrosis-related polypeptide, WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH )
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                                                                                                                                                                                                                                                                            MILLET I.
PEYMAN J A.
KEKUDA R.
JU J.
LI L.
GUO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .284;
-2004
) GENENTECH INC.
40.4%; 5
... 44.6%;
                                                                                                                                                                                                                  PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) GENENTECH INC.
                                                                                                                                                                   ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURAGEN CORP.
                                                 M P
                                                                                                                                                                                                                                                                    Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
in SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I HOSPITAL.
40.4%;
44.6%;
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                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                         40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ein; 253 AA.
antigenic target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 AA
NO:94.
                                                                                                                                                                                                                                                                                                                                                                                                  252
                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
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Pred.
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Pred.
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Pred.
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No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                         553
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555;
No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                        .5; DB
9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
.9e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (hK7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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RESULT
DE PN
                                                                                                                                                                                                                                                                                                                      Best Local Similarity 44.8%;
RESULT 1158
ID AAY77494 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1156
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIT/) SMITHSON G. (MILL/) MILLET I. (PEYM/) PEYMAN J A. (KEKU/) KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
                                                                                                                                                                                                                                                                                    Bovine trypsinogen WO200005384-A1.
                                                                                                                                      AAR53638 standard;
Bovine trypsinogen.
                                                                                                                                                                                                                                                                                                                                                                                                          (GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY08025 standard; protein; Mouse protease-related protebel9736198-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS2004038223-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NOV18a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN62896 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                             PROD-) PRODIGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
1926 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILLER C E.
RASTELLI L.
STONE D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M I
                                      Similarity
                                                                               FILLY & CO
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EISEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALYANKAR U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATTERTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZHONG M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDINGER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATTURAJAN M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽.
                                      ELI.
40.2%;
47.5%;
                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                  40.2%;
                                                                                                                                                                                                                                                                                                                                                                     40.2%;
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43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tein; 253 AA.
protein (PVP)
                                                                                                                                                                                                                                                                                                                             229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA
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Pred.
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Pred.
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Pred.
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                                      No. 1
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No. 9e-
                                                                                                                                                                                                                                                                                                                                                                     No. 9.
                                                                                                                                                                                                       552;
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5; DB
9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5; DB
9e-35;
                                          ۳
                                      DB 2;
.1e-34;
                                                                                                                                                                                                       DB 3;
.1e-34;
                                                                                                                                                                                                                                                                                                                                                                     DB 8;
.8e-35;
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                                                                                                                                                                                                                            229;
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Query Match
Best Local Similarity
RESULT 1161
                                                                                               Best Local
                                                                                                                                                                                      Best Local Similarity
RESULT 1167
                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1164
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RESULT 1162
                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porcine SCCE protein N
W0200262135-A2.
15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                      02-AUG-2001.

02-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

39.8%;

ary Match

39.8%;

46.1%;
                                                                                                                                                                                                                                             AAU23752 standard; protein; 247 AA. Novel human enzyme polypeptide #838. W0200155301-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIL
                                                                Connective tissue US2003054375-A1.
                                                                                                                                                     AAU17043 standard; protein; 247 AA. Human novel secreted protein, SEQ ID W0200155441-A2.
                                                                                                                                                                                                                                                                                                                                                  AAU86677 standard; protein; 247 AA. Novel human connective tissue related
                                                                                                                                                                                                                                                                                                                                                                                                                            AAB35701 standard;
Human trypsin hL au
JP2000253887-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB80953 standard; protein; Bovine met-phe-trypsinogen. WO200119970-A2.
AAW81767 standard; peptide; 223
                                                                                       ADB60011 standard;
                                                                                                                                02-AUG-2001.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                                                        02-AUG-2001.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                      WO200155343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOV18a protein WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA05732 standard; protein;
Human NOV18a protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2001.
(ELIL) LILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                       (TTPH-) TT PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB84420 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                           Local Similarity
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                     Similarity
                                           HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                         hL amino
                                                                                                                                                                                                                                                                                                                                                                                                        .
.
                                                                         ; protein; 247
antigen (CTA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELI.
                  39.8%; (46.1%; )
                                                                                                          39.8%;
46.1%;
                                                                                                                                                                                                  39.8%;
46.1%;
                                                                                                                                                                                                                                                                                                                                                                                  40.0%;
44.0%;
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46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         acid
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sequence.
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NO:92.
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                     Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 552; DB 3; Pred. No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment
                     547.5;
No. 2.6
                                                                                                            547.5; DB 4;
No. 2.6e-34;
                                                                                                                                                                                                   547.5; DB 4
No. 2.6e-34;
                                                                                                                                                                                                                                                                                            547.
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No.
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No. 1
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No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5e-34;
                                                                                                                                                                                                                                                                                            N G
                                                                                                                                                                                                                                                                                            ; DB 4;
.6e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250;
                                                                                                                                                                                                                                                                                                      247;
                                                                                                                                                                                                                                                                                                                                                                                               247;
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Bovine TRYP peptide

fragment

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Best Local Similarity
RESULT 1175
ID AAV91925 standard; p
DE Trypsinogen analogue
PN w0200017332-A1.
PD 30-MAR-2000.
                                        RESULT 1177
ID ADI3715
DE Human p
PN US20031
PD 23-OCT-
RESULT
                                                                                                                        Best Local Similarity RESULT 1176
                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 1173
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RESULT
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Best Local Similarity
RESULT 1170
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                    Query Match
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Best Local :
                                                                                                                                                                               WO2000...
30-MAR-2000.
(ELIL) LILLY & CO ELI.
89.8%; (
                                            Human protease m (Protm),
US2003199010-A1,
23-OCT-200
                                                                                       04-NOV-2003.
04-NOV-2003.
(UYAR-) UNIV ARKANSAS MEDICAL
STY Match
39.7%; S
ery Match
45.8%; I
                                                                                                                                                                                                                                                                                                                        AAR53637 standard;
Bovine trypsin.
EP597681-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRIF PLU-
WO9962004-A1.
02-DEC-1999.
02-DEC-1999.
(MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.
(MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.
39.8%; Score 547; DB 3;
ery Match
39.8%; Score 547; DB 3;
                            (UYAR-) UNIV ARKANSAS.
                                                                                                                                           Human protease
US6642013-B1.
                                                                                                                                                  ADI39734 standard; protein; 244 AA.
Human protease M (proM) protein.
                                                                                                                                                                                                                                 Trypsinogen analogue. WO200017332-A1.
                                                                                                                                                                                                                                                       AAY91925 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                   Cationic bovine trypsinogen WO2003040093-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC73287 standard; protein;
Bovine 2PTC E protein - SEQ
W02003060765-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG31841 standard;
Example protein #3
WO200257954-A1.
                                                                                                                                                                                                                                                                                                   (ELIL ) LILLY &
                                                                                                                                                                                                                                                                                                                                                                                          (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD35545 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AJIN ) AJINOMOTO (UMEY/) UMEYAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MITU ) MITSUBISHI (UMEY/) UMEYAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY69973 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-1998.
(IYAK-) IYAKU BUNSHI
       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                    G
                                                                                                                                                                                                                                                                            39.8%;
46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CO INC.
                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
used in t
    39.7%;
45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHEM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.8%;
46.1%;
                                                                                                                                                                                                                                                                                                                                                                      39.8%;
46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.8%;
46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEKKEI
39.8%;
46.1%;
                                                                       244
                                                                                                                                                                                                                                                        233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              three-dimensional structure analysis method.
                                                                                                                                                                                                                                                                                                                                                                                                                             223 AA.
TRY1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 AA.
) ID 13.
                                                                                             Score 546;
Pred. No. 3
                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                224 AA
    Score 546; DB 8;
Pred. No. 3.3e-34;
                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KENKYUSHO KK.
Score 547; DB 2;
Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                     SCI.
                                                                                                                                                                                                                                                        B
                                                                                                                                                                                    547; DB 3;
No. 2.6e-34;
                                                                                                                                                                                                                                                                                                                                                                     547;
No. 2
                                                                                                                                                                                                                                                                            547; DB 2;
No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              547;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                              DB 8;
                                                                                                                                                                                                                                                                                                                                                                   DB 7;
.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
.5e-34;
              Length
                                                                                                       Length
                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                               223;
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AR-) UNIV ARKANS

LUCY MATCH

Best Local Similarity

RESULT 1182

ID AAY78975 stand-
PN WO2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 1179
ID ADAPTT
                                                                                                                       Query Match
Best Local Similarity
RESULT 1181
                                                                                                                                                Query Match
                                                                                               AAB98502 standard; pro
Human Stratum Corneum
WO200129056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           US2004038223-A1.
26-FEB-2004.
(SMIT/) SMITHSON
(MILL/) MILLET I.
                                                                                                                                                                                                     (SHEN/)
(SHIM/)
(ROTH/)
(LEAC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78974 standard; p
Canine cationic tryp
WO200009739-A1.
24-FEB-2000.
                                                                                                                                               (RIEG/)
(SPAD/)
                                                                                                                                                                       (DIPI/)
                                                                                                                                                                                               (AGEE/
                                                                                                                                                                                                                                                                                                                                            (LILL/)
(GUOX/)
(PATT/)
(SPYT/)
(EDIN/)
                                                                                                                                                                                                                                                                                                                                                                                   (PEYM/)
(KEKU/)
(JUJJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA05742 standard; protein; 247 AA. Human NOV18f protein SEQ ID NO:102. WO2003029424-A2.
                                                                                                                                                                                        (BERG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOV18f
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN62906 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                             ) GANGOLLI E A.
) RIEGER D K.
) SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) FUJI YAKUHIN
                                                                                                                                                                             LEACH M D.
AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                            MILLER C E.
RASTELLI L.
STONE D J.
Similarity
               FUJI YAKUHIN KOGYO KK.
                                                                                                                                                                                                                     PENA C E
SHENOY S
SHIMKETS
                                                                                                                                                                                                                                                                                     GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
                                                                                                                                                                                                                                                                                                                     EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
ORT T.
                                                                                                                                                                                                                                                                                                                                                                                          MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                       EISEN A.
                                                                                                                                                                                                                                                                                                                                                                   guo
                                                                                                                                                                                                                                                                                                                                                   PATTURAJAN M. SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                  SMITHSON
                                                                                                                                                                                                                                                                              CATTERTON E.
                                                             V ARKANSAS.
39.7%;
ilarity 46.5%;
                                       ard; protein;
trypsinogen a
                                                                                                                                                                                                                      ¤ G ≯
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rd; protein;
trypsinogen
                                                                                                                                                                                                                                                                                                                                                                                                                 ດ
                                                                                                      protein; 225 AA.
eum Chymotryptic
                                                                                                                                                                                                              3 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                              39.7%;
45.5%;
39.7%;
44.2%;
                                                                                                                                                                                                              Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOGYO 1
39.7%;
45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 7%;
                                       amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) KK.
; Score
; Pred.
                                              246
Score 545; DB 3;
Pred. No. 4e-34;
                                                              Score
Pred.
                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 AA.
amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 546; DB 6;
Pred. No. 3.3e-34;
                                       AA.
o acid
                                                              545;
No. 3.
                                                                                                                             546; DB 8;
No. 3.3e-34;
                                                                                                     Enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546; DB 3;
No. 3.3e-34;
                                     sequence
                                                              DB 4;
.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                      SCCE,
      Length
                                                                     Length
                                                                                                                                     Length 247;
                                                                                                     catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
       246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247;
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Best Local Similarity
RESULT 1187
ID ADI16686 standard; p:
DE Human NOVX protein to
PN W0200268649-A2.
PD 06-SEP-2002.
Best Local
RESULT 1189
ID ABB78122
                                                                                 RESULT
ID AIT
DE HI
DE H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1184

ID AAW64260 standard; protein; 246 AA.

DE Human amyloid beta-protein precursor inhibitor.
PN W09824886-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PA PR DE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI16686 standard; protein; Human NOVX protein to treat WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stereostructure-related 2PT(
WO2003060765-A1.
24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUSOCCULUM-1998.
11-JUN-1998.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
EXY MATCH
39.5%; Score
39.5%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN42340 standard; protein;
Human novel proteinNOV 62.
US2004033493-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC73299 standard; protein; 220 AA. Stereostructure-related 2PTC_E protein. WO2003060765-A1.
ABB78122 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TCHE/)
(SPYT/)
(ZERH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB21326 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AJIN ) AJINOMOTO (UMEY/) UMEYAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                ) TCHERNEV V T.
) SPYTEK K A.
) ZERHUSEN B D.
) PATTURAJAN M.
) SHIMKETS R A.
                                                                                                                                                            MILLER C E.
GERLACH V.
TAUPIER R J.
GUSEV V Y.
COLMAN S D.
WOLENC A R.
PENA C E A.
PURTAK K.
GROSSE W M.
                                                                                                    ALSOBROOK J P.
LEPLEY D M.
RIEGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUNT SINAI
                                        Similarity
                                                                                 BURGESS
                                                                                                                                                                                                                                                                                                                                                                                                              GANGOLLI
                                                                                                                                                                                                                                                                                                                                                    RASTELLI
                                                                                                                                                                                                                                                                                                                                                                          ANDERSON
                                                                                                                                                                                                                                                                                                                                                                                             PADIGARU
                                                                                                                                                                                                                                                                                                                                                                     Z Z Z Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOSPITAL.
                                      39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.3%;
44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.6%;
44.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.4%;
46.8%;
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  223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 AA.
human pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 544;
Pred. No. !
                                      Score 539.5;
Pred. No. 1.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539.5;
No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541;
No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543;
No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541; DB 7;
No. 7.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5; DB 5;
1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 3;
5e-34;
                                        1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7;
.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
.7e-34;
                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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Best Loca
RESULT 1197
                                                                                                                                                       Best Local Similarity RESULT 1196
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RESULT 1195
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1194
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1190
        Query Match
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                       ADL15205 standard; protein; Pancreatic kallikrein #1. CN1384199-A.
                                                                                                                                                                                                                                                                                          ABB84423 standard; peptide; 249 AA. Murine SCCE protein N-terminal fragment WO200262135-A2.
                             WO200255702-A2.
18-JUL-2002.
                                                  ABG70276 standard; protein; 247 Human Serine Protease TLSP-like
                                                                                                                                                                                                         ABR96164 standard; protein; Human NOV13a protein SEQ ID WO200290568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence US2002072863-A1.
                                                                                                                                                                                                14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                       Kallikrein su
WO9824886-Al
                                                                                                                                                                                                                                                                                                                                                                                                            AAW64261 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              (NISB ) JAPAN TOBACCO INC.
ry Match 38.2%;
t Local Similarity 45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Engraulis japonicus JP2001269173-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB04644 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine SCCE protein WO200262135-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FUIT ) FUJITSU LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Partial trypsin
US2002035434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB83322 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FUIT
                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                      (EGEL/) EGELRUD T. (HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EGEL/) EGELRUD (HANS/) HANSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB84419 standard; peptide;
                                                                                Local Similarity
                                                                                                                                                                                                                                                 ocal Similarity
                                                                               REMIN HOSPITAL SHENZHEN CITY.
h 37.8%; Score 519;
Similarity 44.5%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUJITSU LTD
Similarity
                    CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                   substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۲: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
                                                                                                                                                                                                                                                                                                                                                                                               ; protein; 2 ate binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trypsinogen
                                                                                                                                                                                                                                                                                                                                              38.1%;
43.6%;
                                                                                                                                                                  37.8%;
40.0%;
                                                                                                                                                                                                                                                  38.0%;
43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.7%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.2%;
45.6%;
 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45
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554
                                                                                                                                                                                                                    261 AA
NO:70.
                                                                                                                                                                                                                                                                                                                                                                                                  232 AA.
g site.
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                                                                                                                                              232
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                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                              Score
Pred.
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Pred.
Score
Pred.
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Pred.
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No.
516;
No. 6.
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No. 1.
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No. 1.
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No. 3.9e-32;
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No. 1.6e-32;
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No. 1.
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No. 4.3e-33;
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DB 5;
.9e-32;
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.8e-32;
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Query Match
Best Local S
RESULT 1205
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Best Local Similarity
RESULT 1206
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Best Local S
RESULT 1201
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RESULT 1204
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Best Local S
RESULT 1199
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RESULT 1202
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                                                 Human KLK-L1 protein #2. WO200053776-A2.
                                                                                               O2-UNN-2000.
O2-UNN-2000.
(FUSO) FUSO PHARM IND LTD.
GETY MATCh
Gimilarity 43.5%;
                                                                                                                                             Human neurosin amino acid sequence. WO200031284-Al.
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(HOFF) HOFFMANN LA
(SINO-) SINOGENOMAX
                                                                                                                                                                                                                                       05-DEC-2002
                                                                                                                                                                                                                                                 ABR41530 standard; I
Human DITHP protein
WO200297031-A2.
                                                                                                                                                                                                                                                                                                                                                          ADQ30589 standard; protein; 247 AA. Pancreas cancer marker - trypsin II W02004055519-A2.
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ry Match 36.5%; Score :

t Local Similarity 43.3%; Pred. 1
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN99594 standard; protein;
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14-FEB-2002.
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Human kallikrein.
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                                MOUNT SINAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JAPAN TOBACCO
        HOSPITAL.
36.2%;
43.1%;
                                                                                                                                                                                                                                                        protein; 261 AA.
n modification/maintenance protein.
                                                                                                                                                                                                                                                                                            ROCHE & CO AG F.
CO LTD CHINESE NAT HUMAN GEN.
36.5%; Score 501; DB 8; I
43.3%; Pred. No. 9.8e-31;
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43.3%;
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43.3%;
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trypsinogen
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36.7%;
45.9%;
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37.4%;
46.4%;
                                                                                                                                                                                                                                                                                                                                                                     trypsin II precursor.
                                                                               254
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e #410.
        Score
Pred.
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Pred.
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Pred. No. 1.
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No. 1e-30;
          498; DB 3;
No. 1.7e-30
                                                                                                     500; DB 3;
No. 1.1e-30;
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No. 9
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No.
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No. 5.
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.8e-31;
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.8e-31;
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.6e-31;
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.1e-31;
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                    254;
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Query Match
Best Local Similarity
RESULT 1208
ID AAU69819 standard; p
DE Human prostate cDNA
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                       ABB95279 standard; protein;
Human P703P putative full le
US2002022248-A1.
21-FEB-2002.
                                                                                                                                                                             (DBAS/)
(FOYT/)
                                                                                                                                                                                                                                                                                                                                                      ABU71710 standard; protein; 254 AA.
Prostate cancer specific antigen P703P #7.
US2002192763-A1.
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Human prostate-specific ami
WO200134802-A2.
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                                                                                                                                                             Local Similarity
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WANG A.
SKEIKY Y A V
HEPLER W T.
                                                                                                                                                                           ) HOUGHTON R L.
) Y DE BASSOLS
) FOY T M.
                                    STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                               SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                           JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
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RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
                              CARTER D.
                                                                                                 MITCHAM J
                                                                                                        DILLON D C.
                                                                                                                                                                                                                                       CARTER D.
LI S X.
WANG A.
                                                                                                                                                                                                                                                                                                                 DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                         HARLOCKER
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43.1%;
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43.1%;
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protein
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Pred. No. 1.
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acid
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No. 1.
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No. 1.7e-30;
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.7e-30;
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.7e-30;
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.7e-30;
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RESULT 1214
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RESULT 1213
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Prostate tumour specific protein sequence SEQ ID
W0200289747-A2.
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03-OCT-2002.
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ry Match 36.2%; Score 
t Local Similarity 43.1%; Pred.
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Human KLK4 protein
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                                                                                                                                              (VEDV)
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TY Match 36.2%; Score
Local Similarity 43.1%; Pred.
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1218
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                     CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                HANG Y.

KALOS M D.

FANGER G R.

RETTER M W.

STOLK J A.

DAY C H.

VEDVICK T S.
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HARLOCKER S
   HENDERSON
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SEQ ID NO:13.
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43.1%;
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43.1%;
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43.1%;
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43.1%;
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43.1%;
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protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ein; 254 AA.
polypeptide #60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1079
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Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 7
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P703P.
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No. 1
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No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498; DB 6;
No. 1.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; DB 6;
. 1.7e-30;
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.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7;
.7e-30;
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.7e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254;
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Query Match
Best Local Similarity
RESULT 1219
ID ADI1726 standard; p
DE Polypeptide homologo
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
RESULT 1222
                                                                                                                                          Best Local Similarity RESULT 1223
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RESULT 1221
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  Query Match
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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(HOUG/)
(DBAS/)
(FOYT/)
                                                                              Amino acid sequence WO2004019878-A2.
                                                                                                                                                                                                                                                              ADL27345 standard; peptide; 280 AA. Amino acid sequence of trypsinogen. W02004019878-A2.
                                                                                                                         ADL27346 standard;
                                                                                                                                                                                                   (COMP-) COMPOUND (AFEY/) AFEYAN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypsin-like serine US2003170630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide homologous WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI17276 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide homologous WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                          (SMIT/)
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                                                             L1-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCIO/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
EDINGER S R.
GUNTHER B.
MILLET I.
SCIORE P.
SCIORE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HURAL J.

MCNEILL P D.

HOUGHTON R L.

Y DE BASSOLS ()

FOY T M.
                     COMPOUND
AFEYAN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIU X.
                                                                                                                                                                                                   THERAPEUTICS INC.
                   THERAPEUTICS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) т.
                                                                                                 peptide; 461 AA.
e of trypsinogen-0aa-sp55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease
                                                                                                                                                             36.2%;
42.7%;
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47.4%;
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47.4%;
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47.4%;
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43.1%;
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  36.2%;
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                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                               Score
Pred.
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Pred.
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Pred.
  Score 497.5;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOVX
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                                                                                                                                                                                                                                                                                                                                               497.5;
No. 1.7
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No.
                                                                                                                                                                                                                                                                                                                                             1.7e-30;
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7.6e-30;
                                                                                                                                                               N 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
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                                                                                                                                                               le-30;
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Length 461;
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Best Local Similarity RESULT 1231
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Best Local Similarity
RESULT 1230
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RESULT 1228
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Best Local Similarity
RESULT 1227
                                                                                                                                       Query
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RESULT 1225
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                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Human prostase WO200104143-A2. 18-JAN-2001.
                                                                                                                                                                                                   AAW60592 standard; protein; 248 AA. Human prostate-specific kallikrein W09820117-A1.
                                                                  AAY72524 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein sequence of prostase homologue W0200200708-A2. 03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU74932 standard;
                                                                                                                                                           (INCY-) INCYTE PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostase antigen WO200104143-A2. 18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOUN ) MOUNT SINAI HOSPITAL.

"XY Match 36.2%;

It Local Similarity 43.1%;
                                                                                                                                                                                      4-MAY-1998
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Human prostase antigen #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostase. WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
TY Match 36.2%; Score 497; DB 5;
Local Similarity 43.1%; Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostase. WO200053776-A2.
                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB21320 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COMP-) COMPOUND
(AFEY/) AFEYAN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL27348 standard; peptide; 485 AA. Amino acid sequence of trypsinogen-20aa-sp55. WC200401987-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COMP-) COMPOUND THERAPEUTICS INC (AFEY/) AFEYAN N B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL27347
                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                         protein;
igen #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 254
e of prostase
                                                                                                          4 INC.
36.1%;
43.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HOSPITAL.
36.2%; ;
43.1%; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; 464 AA.
e of trypsinogen-3aa-sp55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.2%;
43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.2%;
42.7%;
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42.7%;
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                                                                248 AA
                                                                                                       Score
Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 497; DB 4;
Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                AA.
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                       496.5; DB 2;
No. 2.2e-30;
                                                                                                                                                                                                                         (HPSK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497;
No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497; DB 3;
No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497.5;
No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5e-30;
                                                                                                                                                                                                                                                                                              DB 5;
.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                             fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8;
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                                                                                                                                                                                                                                                                                                                  254;
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PN DE

standard;

protein;

254

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Best
RESULT
ID AA
                                                                                                                                                                                                       Query Match
Best Local S
RESULT 1239
                                                                                                              Best Local Similarity RESULT 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
RESULT 1234
                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1238
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1233
ID AAU74770 standard;
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                           Pancreas cancer marker - trypsin WO2004055519-A2.
                                                                                                                                                                   ABR54241 standard; protein;
Human NOV35c protein SEQ ID
W02003023001-A2.
                                        (HOFF ) HOFFMANN LA (SINO-) SINOGENOMAX
                                                                                                 ADQ30588 standard; protein;
                                                                                                                                                20-MAR-2003
(CURA-) CURA
                                                                                                                                                                                                                                                   ABR54239 standard; protein;
Human NOV35a protein SEQ ID
WO2003023001-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human trypsinogen partial protein. W02004078777-A2.
                                                                                                                                                                                                                                                                                                       (MOUN ) MOUNT SINAI HOSPITAL.

"Y Match 36.0%;

"t Local Similarity 41.9%;
                                                                                                                                                                                                                                                                                                                                                       Human trypsinogen. WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                          AAB21321 standard;
                                                                                                                                                                                                                                                                                                                                                                                                (BIOR-) BIOREXIS PHARM CORP.
ry Match 36.0%;
t Local Similarity 41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L.
            Local Similarity
1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200261131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequ
WO200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU74931 standard; protein; 248 Amino acid sequence of prostase
                                                                                                                                                                                                                                                                                                                                                                                                                                      6-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG76997 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002.
(SMIK) SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU74770 standard; protein; Protein sequence of prostase W0200200708-A2.
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                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                             CURAGEN CORP.
                                                                                                                                                                                                                                        CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITHKLINE BEECHAM BIOLOGICALS CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d; protein; protein var
                  A ROCHE & CO AG F.

( CO LTD CHINESE NA

36.0%; Score 49

41.9%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BEECHAM BIOLOGICALS.
36.1%; Score 496.5;
43.4%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BEECHAM BIOLOGICALS.
36.1%; Score 496.5;
43.4%; Pred. No. 2.:
                                                                                                                      36.0%;
41.9%;
                                                                                                                                                                                                                36.0%;
41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.0%;
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43.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ein; 262 AA.
n variant #1.
                                                                                              247
                                                                                                                                                                               247 AA.
NO:150.
                                                                                                                                                                                                                                                                        247 AA.
NO:146.
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                                                                                                                      Score
Pred.
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se homologue
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Pred.
                                                                                                                                                                                                                                                                                                         Score
Pred.
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Pred.
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Pred.
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                                                                                            A.
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Pred. No. 2.2e-30;
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A
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                  NAT
494
No.
                                                                                                                      494
No.
                                                                                                                                                                                                                494
No.
                                                                                     precursor.
                                                                                                                                                                                                                                                                                                       494.5; DB 3;
No. 3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495;
No.
                                                                                                                                                                                                                                                                                                                                                                                                494
No.
                 T HUMAN GE
1.5; DB 8
3.1e-30;
                                                                                                                      1.5; DB 6;
. 3.1e-30;
                                                                                                                                                                                                                .5; DB 6;
3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                .5; DB 8
3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 5;
3e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 5;
.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 5;
                         GEN
                                                                                                                                 6
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                                                                                                                             Length
                          Length
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                                                                                                                               247;
                                                                                                                                                                                                                         247;
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-) CORIXA COR.
-y Match
-y Match
-sest Local Similarity
RESULT 1243
ID AAG99058 standa
DE Human prost
PN WC20017
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RESULT 1242
    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate-specific matu WO200134802-A2.
                                                                                                                                                                                                                                                                                                                                                                            ABB95278 standard; protein; 254 AA.
Human P703P mature protein SEQ ID NO 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DBAS/) Y DE BASSOLS C V. (FOYT/) FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU71709 standard; protein; Prostate cancer associated I US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU69818 standard; protein;
Human prostate cDNA encoded
                                                                                                                                        (STOL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cDNA WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate-specific amino acid mature form of P703P. W0200151633-A2.
                                                                                                                                                                                                                                                        (XUJJ/) XU J.
(DILL/) DILLON D C.
(MITC/) MITCHAM J L.
(HARL/) HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                           JS2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
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                                                                                                                        VEDV,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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WANG A.

SKEIKY Y A W.

HEPLER W T.

HENDERSON R A.
                                                                                                                 STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                             JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
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SKEIKY Y A W.
HEPLER W T.
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DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                              CARTER D.
LISX.
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LI S X.
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HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCNEILL P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        36.0%;
42.7%;
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42.7%;
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42.7%;
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42.7%;
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protein
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 494;
Pred. No. 3
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Pred.
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Pred.
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No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494; DB 4;
No. 3.5e-30;
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No. 3.5e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; DB 4;
3.5e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254;
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Query Match
Best Local S
RESULT 1246
                   Query Match
Best Local Similarity 40.4%; Pred. No.
RESULT 1253
ID ADQ39654 standard; protein; 262 AA.
DE Human myocardial infarction-associated
PN W02004058052-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 1249
                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                         Human pancreatic kallikrein. CN1384199-A. 11-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate-specific poly US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR54390 standard; protein; Prostate tumour specific prowo200289747-A2.
                                                                                                                                                                                              Human kallikrein
US2004033582-A1.
                                                                                                                                                                                                                                           (REMI-) REMIN HOSPITAL SHENZHEN CITY.

25 xy Match 36.0%; Score 49

15 Local Similarity 40.4%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOUN ) MOUNT SINAI HOSPITAL.

"ITY Match 36.0%;

It Local Similarity 40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                     ABG76996 standard; protein; 262 AA.
Human kallikrein protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB21319 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human mature pro
US2003185830-A1.
                                                                                                                                                                                                                      ADL64969 standard; protein;
                                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                                             WO200261131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB13973 standard;
                                                                                                                                                  (EDMO/) EDMONDS M. (HUIL/) HUI L. (PERR/) PERRONE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                             RAMA/)
                                                                                                  POWELL J R.
RAMANATHAN C S.
SWANSON B.
TSUCHIHASHI Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORIXA CORP.
APPLERA CORP
                                                                                          ZERBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate
                                                                                        <u>.</u>
                                                                                                                                                                                                          protein (KLK1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                 36.0%;
40.4%;
                                                                                                                                                                                                                                                                                                                                       36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%;
42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%;
42.7%;
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42.7%;
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42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ein; 254 AA.
polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254
                                                                                                                                                                                                                      262 AA.
                                                                                                                                                                                                                                                                                                                  262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                      Score 494;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 494; DB 3; Pred. No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 494; DB 7;
Pred. No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 494; DB 7; Pred. No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 494;
Pred. No. 3
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.
                                                                 9 494;
No. 3.
                                                                                                                                                                                                                                             No. 3.
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No. 3.
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                                gene
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                                                                 DB 8;
.6e-30;
                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                             DB 7;
.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                derived protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                  Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                           Length
                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254;
                                  SEQ ID
                                  1317
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y Match

Aest Local Similarity

RESULT 1261

ID ABP74711 stand-
DE Human gland-
PN W02002-
PD 17-
PA
                                                                Best Local Similarity RESULT 1262
                                                                                                                                                                                                                         Best Local Similarity RESULT 1260
                                                                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 1259
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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Best Local Similarity
RESULT 1256
                                                             RESULT 1255
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                  Pancreatic )
CN1384199-A.
                                       ADL15204 standard; protein;
Pancreatic kallikrein #1.
                                                                                                                    ABP74711 standard; protein;
Human glandular kallikrein j
                                                                                                                                                                                         AAW71005 standard; protein; 262 AA.
Human prostate-associated kallikrein
W09832865-A1.
                                                                                                                                                                                                                                              14-SEP-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                 AAB21324 standard; protein; 258 AA.
Human EMSP.
                                                                                                                                                                                                                                                                       WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                  Human EMSP. WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                     AAB21308 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        ADN04297 standard; protein; 247 AA. Antipsoriatic protein sequence #343 WOZ004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human trypsinogen. WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOUN) MOUNT SINAI HOSPITAL.
ry Match 35.9%;
t Local Similarity 42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB21316 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human trypsinogen WO2003023001-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS34891 standard; protein; 262 l
Human autoimmune disease-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-2004 (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR54277 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004083403-A2.
                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                               284;
-2004.
) GENENTECH INC.
35.9%; (
35.2%; (
42.1%;
   REMIN HOSPITAL S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; protein; 240 AA.
protein SEQ ID NO:341.
                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                           HOSPITAL.
35.9%; !
42.8%; !
                                                                                                                                                 1 INC.
35.9%;
40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                              35.9%;
42.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.9%;
42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.0%;
40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.0%;
40.4%;
 SHENZHEN CITY.
5.9%; Score 493;
                                                                    S CORP.
Score
Pred.
                                                   262
                                                                                                                              262
                                                                                                                                                                                                                                                                                                                                                                      253
                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                    precursor
                                                                                                                                                                                                                              Score
Pred.
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Pred.
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Pred.
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Pred. No. 3.0
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Pred.
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Pred.
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d protein
                                                                     493; DB 6;
No. 4.3e-30;
                                                                                                                                                 493;
No. 4
                                                                                                                                                                                                                             493;
No. 4
                                                                                                                                                                                                                                                                                                           493;
No. 4
                                                                                                                                                                                                                                                                                                                                                                                       493; DB 8;
No. 4.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493.5; DB 6
No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494;
No. 3.
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No. 3.
                                                                                                                                                                                                designated
                                                                                                                                                                                                                             4.2e-30;
                                                                                                                                                                                                                                                                                                         ; DB 3;
4.2e-30;
                                                                                                                   protein
  BB
                                                                                                                                                DB 2;
.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8;
.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
.6e-30;
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 7;
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                                                                                                                   SEQ
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Length
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                                                                                                                   IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                   NO:600
                                                                                                                                                          262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241;
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Best Local Similarity
RESULT 1270
ID ABG77002 standard; p
DE Human kallikrein 1 p
PN W0200261131-A2.
PD 08-AUG-2002
PA (BRIM ) BRISTOL-MYER
PA (TSUC/) TSUCHIHASHI
PA (HUIL/) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best .
RESULT 1
                                        Query Match
Best Local Similarity
RESULT 1271
                                                                                                                                                                                                                                     Best Local Similarity
RESULT 1269
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RESULT 1263
ID ADM72846 standard; p
DE Human glandular kall
PN WO2004022709-A2.
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
RESULT 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 1266
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RESULT 1265
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                   ABG76998 standard, p
Human kallikrein pro
WO200261131-A2.
08-AUG-2002.
Human NOV18g protein SEQ ID WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOZUVAL-2001.
26-APR-2001.
(UYAR-) UNIV ARKANSAS.
(WARTCH 35.8%; §
                                                                                                                 ABG77002 standard; protein; 262 AA. Human kallikrein 1 polymorphic sequ W0200261131-A2.
                                                                                                                                                                                                    Human pancreatic WO200055320-A1.
                                                                                                                                                                                                             AAB54293 standard; protein; 267 Human pancreatic cancer antigen
                                                                               (BRIM ) BRISTOL-MYERS (TSUC/) TSUCHIHASHI Z.
                                                                                                                                                                                (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                 (TSUC/) TSUCHIHASHI (HUIL/) HUI L.
                                                                                                                                                                                                                                                                                                                                                                              04-JAN-1989.
(AMGE-) AMGEN.
                                                                                                                                                                                                                                                                                                                                                                                                    Kallikrein encoded EP297913-A.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAP95121 standard;
                                                                                                                                                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIBB (TSUC/) TSUCHIHASHI Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TRYI trypsinogen variant WO9910503-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 35.8%;
Local Similarity 41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB21315 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW93488 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB98503 standard; protein; 225 AA.
Human trypsin serine protease catalytic
WO200129056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human glandular kallikrein:
WC2004022709-A2.
18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MANN-) MANNKIND CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROCHE DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                       i; protein;
protein vai
                                                                                                                                                        35.8%; 9
40.4%; 1
                                                                                                                                                                                                                                                                                                                                                                                                            protein; 262 AA.
by clone lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                35
40.
                                                                                                                                                                                                                                             35.8%;
40.4%;
                                                                                                                                                                                                                                                                                                                                                       35.8%;
40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.8%;
43.7%;
                                                                                        SQUIBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.9%;
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                                                . 48;
                                                                                                                                                                                                                                                                                                                       in; 262 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GMBH.
3%; Score
7%; Pred.
                224 AA.
NO:104.
                                               Score
Pred.
                                                                                                                                                        Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256
                                                                                           8
                                                                                                                                                                                                                                             Score 492;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 AA.
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Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 AA.
protein
                                                                                                                         sequence
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                                                                                                                                                                                                                                                                                                                  ? AA.
t #2.
                                                                                                                                                                                                            AA.
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
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                                                                                                                                                        492;
No. 5.
                                               491;
No. 6.
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"n. 4.
                                                                                                                                                                                                                                                                                                                                                      No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            492;
No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    492;
No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493;
No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 3;
5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.4e-30;
                                                                                                                                                                                                            sequence
                                               DB 5;
.2e-30;
                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3e-30;
                                                                                                                                                                                                                                            DB 5;
.2e-30;
                                                                                                                                                                                                                                                                                                                                                       DB 1;
.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
1.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
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                                                       Length
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                                                                                                                                                                                                            SEQ
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                                                                                                                                                                                                            IJ
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                                                                                                                                                                                                            NO:745
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Match

Best Local Similarity

RESULT 1274

ID AAY25510 stand

DE Human pro-

PN EP936
                                                     RESULT
ID AD
DE An
PN WO
PD 08
                     Best Local Similarity
RESULT 1276
                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1273
                                                                                                                                                                                                                                            Best Local Similarity RESULT 1272
                                                                                            Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                   AAY25510 standard; protein;
Human prostate serine protes
                                                            ADN04726 standard; protein; 247 AA.
Antipsoriatic protein sequence #544.
W02104028479-A2.
                                                                                                                                                                                           Human serine pr
WO200125446-A1.
                                                                                                                                                                                                        AAE00397 standard;
ADN99593 standard; protein; 2 Novel human protein sequence WO2004038003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                (GUOX/)
(PATT/)
(SPYT/)
(EDIN/)
(ELLE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV18g.
US2004038223-A1.
                                                       08-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (/TTIMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN62908 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-)
                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                            SPAD/)
                                                                                     Local Similarity
1275
                                                                                                                                                                                                                                        AGEE M L.
BERGHS C.
DIFIPO V A.
EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILLET I.
) PEYMAN J A.
) KEKUDA R.
) JU J.
) LI L.
                                                                                                                                                                                                                                                                                               MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M I
LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                               ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
                                                                                                             BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURAGEN
                                                                                                                                                                                                                                                                                                                                                                         CATTERTON E
                                                                                                                                                                                                                                                                                                                                                                                                        GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                       MALYANKAR U M.
                                                                                                                                                                                                   protease,
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                                                                                                                                                                                                           protein;
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45.3%;
                              35.5%;
42.3%;
                                                                                            35.6%;
43.9%;
                                                                                                                                                           35.6%;
43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.7%;
45.3%;
                                                                                                                                   protease protein
                                                                                                                                                                                                   PROST 07.
       247 AA.
e #409.
                                                                                                                                            231 AA.
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                              Score
Pred.
                                                                                             Score
Pred.
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Pred.
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Pred.
                                                                                                                                                           Score 489.5; DB 4;
Pred. No. 7.2e-30;
                               488;
No.
                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 6
                                                                                                                                                                                                                          490; DB 8;
No. 6.3e-30;
                                                                                            8.4e-30;
                               9.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3e-30;
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                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                 Length
                                                                                                    Length 231;
                                                                                                                                                                   Length 234;
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Best Local Similarity
RESULT 1277
ID AAMATA
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RESULT 1278
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Best Local
RESULT 1280
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RESULT
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           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU71763 standard; p
Prostate cancer spec
US2002192763-A1.
19-DEC-2002.
                                                                                                                                                                     (XUJJ/)
(DILL/)
(MITC/)
                                                                                                                                                                                                      Human P703P/PSA
US2002022248-A1.
21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU69872 standard; protein; 449 AA. Human prostate serum antigen/P703P W0200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM01227 standard; protein; 449 AA. P703P and PSA fusion amino acid sequence
                                                                                                                                                                                                                          ABB95332 standard; protein;
Human P703P/PSA fusion prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FIVE-) FIVE PRIME THERAPEUTICS INC. sry Match 35.5%; Score 4 tocal Similarity 42.3%; Pred. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                               (MCNE,
                                                                                                                                                                                                                                                                                                      HOUG
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 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                               STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W
HEPLER W T.
                                                                                                                                                                                                                                                                                        HURAL J.

MCNEILL P D.

HOUGHTON R L.

Y DE BASSOLS C V
                                                                                                                                                                                                                                                                                                                                WANG A.

SKEIKY Y A W.

HEPLER W T.

HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITCHAM J L.
HARLOCKER S
                                                                                                                                                          DILLON D C.
MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                       JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                 JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                         Similarity
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                    HENDERSON R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rd; protein; 449 P
specific antigen
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35.5%;
44.1%;
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44.1%;
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44.1%;
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44.1%;
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protein SEQ ID
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Pred. No. 9
Score
Pred.
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Pred.
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Pred.
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Pred.
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en fusion
 487.5; DB
No. 2e-29;
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No. 2e-29;
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No. 2e-29;
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No. 2e-29;
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9.9e-30;
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           Length
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                                                                                                                                                                                                                                                                      449;
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Query Match
Best Local Similarity
RESULT 1285
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Best Local S
RESULT 1283
                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 1282
ID ADB14067 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1281
                                 (VEDV)
                                                                                                                       US2002192763-A1.
19-DEC-2002.
                                                                                                                                     Prostate
                                                                                                                                            ABU71888 standard; protein;
                                                                                                                                                                                                                  (SKEI/)
(HEPL/)
(HEND/)
                                                                                                                                                                                                    (HURA/)
                                                                                                                                                                                                                                                                                                                                                              ABU71889 standard; protein; Prostate cancer specific ant US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate specific protein US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate-specific US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG26483 standard; protein;
                                                                                                                                                                                                                                                                                                                      (MITC/) MITCHAM J L.
(HARL/) HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR54444 standard; protein; 449 prostate tumour specific protein
                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate tumour
WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
                                                      DILLON D C.
MITCHAM J L.
HARLOCKER S
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                            ) HOUGHTON R L.
) Y DE BASSOLS (
) FOY T M.
                              STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                 WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                      JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                               XU
J
                                                                                                                                                                                                                                                CARTER D.
                                                                                                                                                                                                    MCNEILL P D.
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DILLON D C.
                                                                                                                                     cancer associated
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                                                                                                                                                           35.5%;
44.1%;
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44.1%;
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44.1%;
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44.1%;
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polypeptide
                                                                                                                                                                                                                                                                                                                                                                   antigen fusion protein
                                                                                                                                    ı; 585 AA.
l protein
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                                                                                                                                                           Score
Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 487.5; DB Pred. No. 2e-29;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
P703P/PSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n sequence
                                                                                                                                     #72
                                                                                                                                                           487.5; DB 4;
No. 2.6e-29;
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No. 2e-29;
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No. 2e
                                                                                                                                                                                                                                                                                                                                                                                                                                    #113.
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-29;
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                                                                                                                                                                  585;
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Query Match
Best Local S
RESULT 1290
ID AAY31160
DE Human try
PN US5948892
PD 07-SEP-19
                   Best Local Similarity RESULT 1291
                                                                                                                     Query Match
Best Local;
RESULT 1286
ID ABR54580
DE Prostate
                                                                                                                                                                                                                                                                                                                                                          Best Loca
RESULT 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1287
                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                         (DILL/) DILLUM J L. (MITC/) MITCHAM J L. (MARL/) HARLOCKER S L
ADL15207 standard; protein; Pancreatic kallikrein #3.
                                              07-SEP-1999.
(AMGE-) AMGE
                                                              Human trypsin serine US5948892-A.
                                                                              AAY31160 standard; protein;
                                                                                                                    (DBAS/)
(FOYT/)
                                                                                                                                                                                                                                                                                                                                                                                             Human prostate-specific polypeptide US2003157089-A1.
                                                                                                                                                                (HEPL)
                                                                                                                                                                                                                                                                                                                              ABU71890 standard; protein; 801 AA. Prostate cancer specific antigen fusion protein US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOPP/hPAP fusion protein, FOPP3. US2003185830-A1.
                                                                                                                                                                                                                                                                                                                      19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                21-AUG-2003.
(CORI-) CORIXA CORP.
                                                                                                                                              MCNE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2002.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR54580 standard; protein; 585 Prostate tumour-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR54580 standard;
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(HEND/)
(HURA/)
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                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                             CARTER D.
LI S X.
WANG A.
SKBIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                    STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                              KALOS M D. FANGER G R. RETTER M W.
                                                                                                 Similarity
                                                                                                                   FOY T M.
                                                                                                                          HOUGHTON R L.
Y DE BASSOLS C V.
                                                                                                                                              MCNEILL P D.
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HOUGHTON R L.
Y DE BASSOLS C V
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                                                                                                                                                                                                                                                                                                             XU J.
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HENDERSON R
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44.1%;
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44.1%;
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44.1%;
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44.1%;
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        261
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                         Score
Pred.
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Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 487.5; DB 7;
Pred. No. 2.6e-29;
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Pred.
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Pred.
        AA
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                         487; DB 2;
No. 1.1e-29;
                                                                                               487.5;
No. 3.6
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487.5;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                           #249
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No. 2.6e-29;
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                                                                      domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1020.
                                                                                                ; DB 4
.6e-29;
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2.6e-29;
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.6e-29;
                                                                                                         4.
                                 Length
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                                                                                                        801;
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Lery Match
Best Local Similarity
RESULT 1292
ID ABM83249 stand-
DE Human dia-
PN WO200
DE Part CORP
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ID AAW577.
DE Tryp61
PN JP1009
PD 21-APR
PA (SHIS
                                                       RESULT
ID AA
DE Hu
PN WO
PD 18
PA (S
                                                                                                                                                   RESULT
ID AA
DE Hu
PN WO
PD 05
PA (S
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ID AL
DE Pa
PN CN
PD 11
PA (H
                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1297
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human diagnostic and therapeutic pprotein WO2004023973-A2.
                                                                              Human prostase antigen P703PDE5 sequence. WO200104143-A2.
                                                                                                                                                                                                                                                          AAP70568 standard; pro
Human kallikrein-like
JP62126980-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW57740 standard; protein;
Trypsinogen-like protein.
Up10099080-A.
                                                                                                                                                                                                                                     09-JUN-1987.
(NAKA/) NAKANISHI
                                                                                                                                                                                                                                                                                                                                              Human KLK-L1 pr
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pancreatic kallikrein #2.
CN1384199-A.
  AAU74902 standard; protein; 2
Protein sequence of prostase
                                                                                                                                                                        Human serine pr
WO200123587-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM83250 standard;
                                                                                                                            SMITHKLINE BEECHAM PLC.

(SMIK) 34.8%; Score

ry Match 34.8%; Pred.
                                                                                                                                                                                              AAU01290 standard;
                                                                                                                                                                                                                                                                                                                                                                    AAB21293 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL15206 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REMI-) REMIN HOSPITAL SHENZHEN CITY.
ry Match 35.3%; Score 48
Local Similarity 40.2%; Pred. No
                                                                                                                                                                                                                                                                                                   (MOUN ) MOUNT SINAI HOSPITAL.

CY Match 35.1%;

Local Similarity 42.2%;
                                                                                                                                                                                                                                                                                                                                                                                       (REMI-) REMIN HOSPITAL SHENZHEN CITY
CY Match 35.2%; Score 48
Local Similarity 39.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1998.
(SHIS ) SHISEIDO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE CORP.
                                                      SMIK ) SMITHKLINE BEECHAM BIOLOGICALS (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-MAR-2004
                                                                                                                    Local Similarity
1299
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1295
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                                                                                                                                                                                                                ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                        ndard; protein;
protein #1.
                                                                                                                                                                                  protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d; protein; 333 A and therapeutic
                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                             protein;
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35.2%;
42.5%;
                                 34.8%;
43.8%;
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43.5%;
                                                                                                                                                                                                                35.0%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.2%;
43.5%;
                                                                                                                                                                                  otein; 216
HETAA37p.
                                                                                                                                                                                                                                                                       substance
                                                                                                                                                                                                                                                                                                                                                                   237
  226 AA.
e homologue #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 484.
Pred. No.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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c pprotein
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has
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No. 3
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                                  477.5; DB 4;
No. 5.8e-29;
                                                                                                                                                                                                                                                                                                      482
No.
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No. 3
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No. 2.1e-29;
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No. 2.1e-29;
                                                                                                                               477.5; DB 4;
No. 5.5e-29;
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                                                                                                                                                                                                                                                                     hypotensive
                                                                                                                                                                                                                  L; DB 1;
. 3.6e-29;
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1.9e-29;
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                                                                                                                                                                                                                                                                                                      .5; DB 3;
2.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
.5e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 261;
                                            Length
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Best L
RESULT 1
                               Query Match
Best Local Similarity
RESULT 1306
                                                                         Best Local
RESULT 1304
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                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence
WO200200867-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200104143-A2.

18-JAN-2001.

(SMIK ) SWITHKLINE BEECHAM BIOLOGICALS (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY72522 standard; protein; 312
NS1-P703P-His fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU74933 standard; protein; 226 AA.
Amino acid sequence of prostase protein
WO220200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200200708-A2
Human diagnostic
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                              Human prostate s
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                  ABU71886 standard;
                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                     AAU74929 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

ry Match 34.8%; Score 477.5; DB 5;
t Local Similarity 43.8%; Pred. No. 8.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74768 standard; protein; 312 AA.
Amino acid sequence of wild-type NS1-p703-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                     ABM82601 standard;
                                                                (FOYT/)
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MITCHAM J L.
HARLOCKER S !
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                               SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                WANG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMITHKLINE
                                                              FOY
                                                                       HOUGHTON R L.
Y DE BASSOLS C V.
                                                                                                                                                                                                                                                                                                                                                                           SMITHKLINE
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                                                                                             HURAL J.
MCNEILL P D.
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                                                                                                                                                                                                                                                                                                                       specific
          1; protein; 239 F
and therapeutic
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43.8%;
                                                                                                                                                                                                                                                                                                                                                     BEECHAM BIOLOGICALS
34.8%; Score 477
43.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                         protein; 312 AA.
e of wild-type NS1-P703P-His
                                                                                                                                                                                                                                                        ۲
                                        34.8%;
43.8%;
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43.8%;
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43.8%;
                                                                                                                                                                                                                                                                                                                      antigen
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#; Score 477.

#; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 477.5; DB 4
Pred. No. 8.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 477.5;
Pred. No. 5.
                                        Score 477.5; DB 4;
Pred. No. 8.9e-29;
                     A
                                                                                                                                                                                                                                                                                                                        (PSA) epitope #26
          pprotein
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5.8e-29;
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                                                                                                                                                                                                                                                                                                                                                        ; DB 5;
3.1e-29;
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.8e-29;
            SEQ
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            NO:2850
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                                                                                                                                                                                                                                                                                                                                                                                                         protein.
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RESULT
ID AA
DE Hu
PN WO
PD 12
PA (C)
                                                                                                                                            Best Local Similarity RESULT 1314
                                                                                                                                                                                                                         RESULT 1313
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RESULT 1310
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Best Local S
RESULT 1307
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RESULT 1309
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RESULT 1308
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                               Human P703P inv
WO200125273-A2.
                                       AAG62147 standard; protein;
Human P703P inventive antige
                                                                                                           AAG99008 standard; protein;
Human prostate-specific amin
WO200134802-A2
                                                                                                                                                                                           Prostate tumour antigen predicted WO200125272-A2.
                                                                                                                                                                                                          AAB74806 standard; protein;
                                                                                                                                                                                                                                                                       AAU69768 standard; |
Human prostate cDNA
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                               Human prostate-specific amino acid WO200151633-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200004149-A2.
                                                                                        CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004.
(FIVE-) FIVE PRIME THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human diagnostic and therape

9-MAR-2004.
                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY82008 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human protein WO2004038003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN99649 standard; protein;
                                                                                                                                                                                                                                                                                                                                 CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM82603 standard;
                                                                                                                                                                                                                                                                                                                                                                                                               CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2004
                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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           CORIXA CORP.
                                                                                                                                                                     CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d; protein; 239 AA.
and therapeutic pprotein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; protein; 220 AA.
prostate tumour protein
                                                                                                                                                                                                                                                                                 protein;
A encoded
                                                                     34.4%;
                                                                                                                                                  34.4%;
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  34.4%;
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43.8%;
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43.8%;
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                                      otein; 220 AA.
antigen SEQ ID
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40.1%;
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40.1%;
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40.1%;
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Protein
                                                                                                                               220
                                                                                                                                                                                                            220 AA
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e #465.
                                                                   Score 472.5; DB 4;
Pred. No. 1.4e-28;
  Score
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Pred.
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Pred.
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Pred.
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Pred. No.
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Pred.
                                                                                                                    20 AA.
acid
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Pred.
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Pred. No.
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Pred.
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c pprotein
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 472.5;
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No. 1.4e-28;
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No. 1.4e-28;
                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                            472.5;
No. 1.4
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473;
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No. 8.8e-29;
                                       NO:
                                                                                                                                                                                                                                                                               #8
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No. 8.8e-29;
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                                                                                                                                                                                                  acid
                                       330.
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.6e-28;
 В
                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
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                                                                                                                    P703PDE5
                                                                                                                                                                                                                                                                                                                                                             P703PDE6
                                                                                                                                                                                                 sequence
4;
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Length
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                                                                            220;
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PR DE

BB

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Best Local Similarity
RESULT 1320
ID ADG26193 ~'
DE "...
                                                           Best Local Similarity
RESULT 1319
ID ADB13777 standard; p
DE Human prostate speci
PN US2003185830-A1.
PD 02-OCT-2003.
                                                                                                                             Query Match
Best Local Similarity
RESULT 1318
ID ABR54340 standard; pro
DE Prostate tumour specif
PN W0200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1316
ADG26193 standard; protein; 220 AA.
Human prostate-specific polypeptide
                                            02-OCT-2003.
(CORI-) CORIXA CORP.
                                                                                                                                             ABR54340 standard; protein; 220 AA. Prostate tumour specific protein sequence W0200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                           ABB95228 standard; protein;
Human P703PDE5 protein SEQ
                                                                                                                                                                                                           (HEND/)
                                                                                                                                                                                                                                                                                                                                                                                     US2002022248-A1.
                                                                                                                                                                                                                                                                                                                   KALO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HEPL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU71659 standard; protein;
Prostate cancer specific ant
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LI S X.
WANG A.
SKEIKY Y A W
HEPLER W T.
HENDERSON R
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FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
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HARLOCKER S
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) WANG A.
) SKEIKY Y A W.
) HEPLER W T.
HENDERSON R A.
                                                                                                                            CORIXA CORP.
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VEDVICK T S.
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KALOS M D.
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MITCHAM J L.
HARLOCKER S 1
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Y DE BASSOLS C
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43.8%;
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43.8%;
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protein
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ID NO 327
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en P703P
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Pred.
                           Score 472.5; DB 7
Pred. No. 1.4e-28;
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Pred. No. 1.
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P703PDE5.
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No. 1.4e-28;
#9
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WORCESTER 1

Hest Local Similarity

RESULT 1328

ID AAY56048 stand

DE Human pro-

PN W099-

PD W099-
Query Match
Best Local Similarity
RESULT 1329
ID AAY77842 standard; p
Human prostate-speci
PN WO9960984-A2.
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RESULT 1321
ID ADI39732 standard; p
DE Human glandular kall
PN US6642013-B1
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ID ABR9616
DE Human N
PN WO20029
PD 14-NOV-
PA (CURA-)
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ID ADI3715
DE Human g
PN US20031
PD 23-OCT-
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Prostate specific !
WO200145728-A2.
                                                                                                                                                            Human prostatic specific WO9711172-A1.
                                                                                                                                                                                                                                                                                                                                                                                        04-JAN-1989.
(AMGE-) AMGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAP92314 standard; protein;
Human recombiant kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR96163 standard; protein;
Human NOV12a protein SEQ ID
WO200290568-A2.
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US2003199010-A1.
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Human glandular kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI39732 standard; protein; 262 AA.
Human glandular kallikrein (Hk2) protein.
US6642013-B1.
                                                                                                                                                                                AAW13649 standard; protein;
                                                                                        AAY56048 standard; protein; 261 Human prostate-specific antigen.
                                                                                                                                                                                                                                                                                                          (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                   AAB21313 standard;
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                                                           (UYPE-) UNIV
                                                                                                                                                                                                                          EPIM-) EPIMMUNE INC.
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34.2%;
ilarity 40.4%;
         especific anti
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34.2%;
40.4%;
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          antigen
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antigen.
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(hHk2)
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NO:68.
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(PSA)
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No. 3
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No.
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No. 1.7e-28;
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No. 1.6e-28;
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2.3e-28;
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2.3e-28;
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2.3e-28;
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2.3e-28;
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2e-28;
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1.6e-28;
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RESULT 1330
                                                                Best Local Similarity RESULT 1335
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14-SEP-2000.

(MOUN ) MOUNT SINAI HOSPITAL.

(MOUN ) MOUNT SINAI HOSPITAL.

34-2%;

ery Match 34-2%;
                                                                                                                                                                                                                                                                                                                                                                              Human prostate specific antigen W0200125273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB74821 standard; protein; 261 AA. Prostate tumour antigen amino acid W0200125272-A2.
                                     Human PSA protein WO200281646-A2.
                                                       ABP74202 standard;
                                                                                                                                                                                                                                                                                                    Human prostatic
US2002192763-A1.
19-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate WO200125273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG62144 standard; protein;
Human prostate specific memb
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MITCHAM J L.
HARLOCKER S
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DAY C H.
VEDVICK T S.
CTL IMMUNOTHERAPIES h 34.2%; Similarity 40.4%;
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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KALOS M D.
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Best Local
RESULT 1340
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RESULT 1337
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ID ADB82777 standard;
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23-007-2003.
(UYAR-) UNIV ARKANSAS.
(Watch 34.2%;
                              Human WT1/PSA fusion WO200125273-A2.
                                               AAG62154 standard; protein; 6
Human WT1/PSA fusion protein
                                                                                                                     AAB08449 standard; protein; 375 AA. A human prostate specific antigen vWO200049158-A2.
                                                                                                                                                                                           Tumour-associated WO2004030615-A2. 15-APR-2004.
                                                                                                                                                                                                           ABM82166 standard; protein;
Tumour-associated antigenic
                                                                                                                                                                                                                                                                                                                                                     Human prostate s
US2003199010-A1.
23-OCT-2003.
                                                                                                                                                                                                                                                                                                      ADM72819 standard;
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                                                                                                                                                                                                                                                                                    WO2004022709-A2
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(UYAR-) UNIV ARKANSAS MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate US6642013-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence useful for the WO2003050236-A2.
                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   ADI37157 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI39733 standard; protein; 261
Human prostate specific antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PSA precursor WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ59022 standard; protein;
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(CTLI-) CTL IMMUNOTHERAPIES
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PSA protein #SEQ II
WO2003008537-A2.
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-2003
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                                                                                                                                                                                 GENENTECH INC
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ib 34.2%; Score 470.5; DB 7
Similarity 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                           standard; protein; 261 AA.
protein SEQ ID NO:78.
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Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORP.
Score 470.5; DB 7
Pred. No. 2.3e-28;
                                                                              Score
Pred.
                                                                                                                                                            Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 2.
                                             AA.
                                                                                                                                                                                                                                                                                                                                                                        AA.
(hPSA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
(PSA)
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No. 6.3e-
                                                                                                                             variant
                                                                             470
No.
                                                                                                                                                            470
No.
                                                                                                                                                                                                                                         470.5; DB 8
No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                        470.
No.
                                                                                                                                                                                                                                                                                                                                                                                                     470.
No.
                                                                                                                                                                                                            (TAT)
                                                 ŏ:
                                                                              ယ့်
                                                                                                                                                            .5; DB 8;
2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                        .5; DB 8
2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer (SeqID 1558).
                                                                              .4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 8;
                                                                                                                                                                                                           polypeptide
DB 4;
3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 7
.3e-28;
                                                                                                                            polypeptide
                                                                                       DB
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                                                                                                                                                                                                                                                   8
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        Length
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                                                                                                                                                                                                          PRO2109,
                                                                                       375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261;
                                                                                                                                                                                                          SEQ:5591
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LUEY MATCH
BEST LOCAL SIMILARITY
RESULT 1333
ID AAR82703 Stap?
DE Human par'
PN JP077
                                                                                                                                       Query Match
Best Local Similarity
RESULT 1352
ID AAP81243 standard; p
DE Human spleen trypsin
PN JP63160582-A.
PD 04-JUL-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1345
ID AAB67545 standard; p
DE Amino acid sequence
PN W0200116289-A2.
PD 08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Matc
Best Local
RESULT 1349
                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1351
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
RESULT 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
RESULT 1347
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                           AAU74767 standard; pi
Amino acid sequence o
WO200200708-A2.
03-JAN-2002.
                                                  AAR82703 standard; protein; 2 Human pancreatic trypsin III. JP07184655-A.
                                                                                                                                             Human spleen trypsin III (trysinogen UP63160582-A.
                                                                                                                                                                                                                                                   AAU74928 standard; p
Amino acid sequence
WO200200867-A1.
                                                                                                                                                                                                                                                                                           WOZUUGUGA

03-JAN-2002.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

(SMIK ) SCORE 467.5; DB 5;

34.0%; SCORE 467.5; DB 5;

13.4%; Pred. No. 4.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY72521 standard; protein; 312
NS1-P703P mutated-His fusion pro
WO200104143-A2.
18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU74934 standard; protein; 231 AA.
Amino acid sequence of P703P mutated-His
WC200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK) SMITHKLINE BEECHAM BIOLOGICALS. (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU74903 standard; p
Amino acid sequence
WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PSA precursor WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ59024 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ORTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
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                                                                                                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORTHO-MCNEIL PHARM : tch 34.1%; al Similarity 43.8%;
 Similarity
                          SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                  BEECHAM BIOLOGICALS.
34.0%; Score 467.
43.4%; Pred. No.
                                                                                                                                                                                                                                                                 protein; 312 AA
e of NS1-P703P mu
                                                                                                                                                                                                                                                                                                                                                                 protein; 312
e of NS1-p703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
e of p703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BEECHAM BIOLOGICALS
34.0%; Score 467
43.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 284
e of protease
 34.0%;
40.9%;
                                                                                                  34.0%;
40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                       34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.1%;
40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W INC.

b; Score 469; :

b; Pred. No. 3.
                                                                        247
 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA.
mutated-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 AA.
sequence.
                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
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Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                          A
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mutated-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
MH2 catalytic domain in
                                                                                                                                                                                                                                                                 mutated-His
467; DB
No. 4.1e-
                                                                                                  467; DB 1;
No. 4.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 3.5
                                                                                                                                                                                                                                                                                                                                                                                                     467.5; DB 4
No. 4.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468.5; DB 7;
No. 3.3e-28;
                                                                                                                                                                                                    .5; DB 5
4.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.5; DB 5;
3.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion
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                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231;
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RESULT 1360
ID ADR6627
DE Human p
N WO20040
PN WO21040
PD 10-SEP-
PA (HINZ/)
PA (DAHL/)
PA (ROSE/)
PA (HERM/)
PA (PILA/)
RESULT 1361
ID ADR6699
DE Human F
PN W02.004c
PD 10-SEP-PA (HINZ/)
PA (DAHL/)
PA (ROSE/)
                                                                                                                                                                                                                                            RESULT
ID AII
ID HU
PN WC
PD 10
PA (E
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PA (E
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RESULT 1357
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RESULT 1356
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RESULT 1355
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                                                                                                                                                                                                                      Query
Best L
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                          (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                            ADR66838 standard; protein; Human prostatic carcinoma de WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                  ADM12395 standard; protein; 261 AA.
Human prostate-specific antigen protein.
US2003235594-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB84422 standard; peptide; Rat SCCE protein N-terminal WO200262135-A2.
                                                                                                                                                                           ADR66277 standard; protein; Human prostatic carcinoma de WO2004076614-A2.
                                          ADR66934 standard; protein; Human prostatic carcinoma dw02004076614-A2.
                                                                                                                                                                                                                                                                                                                                                      (ANTI-) ANTIGEN EXPRESS INC.
ry Match 33.7%;
t Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA50549 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PSA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ59028 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH) US DEPT HEALTH & HUMAN SERVICES ry Match 34.0%; Score 466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003047506-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ59026 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.

TY Match 33.8%; Score 464.5; DB 7
Local Similarity 40.4%; Pred. No. 6.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGEL/) EGELRUD T.
HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CENZ ) CENTOCOR INC.
                                                                                                         ICOSE/) ROSENTHAL A.
IERM/) HERMANN K.
PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
                                                                                      ocal Similarity
                                                                                                                                                                                                                     ocal Similarity
                                                                                                                                            /) HINZMANN B.
                     HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 261 AA.
(Y154) precursor protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 261 AA. (L155/Y154) precursor protein
                                                                                      33.7%;
40.2%;
                                                                                                                                                                                                                      33.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             33.8%;
42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.8%;
42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ein; 237 AA.
specific antigen (PSA/KLK3),
                                                                                                                                                                                       n; 248 AA.
derived p
                                                                                                                                                                                                                                                                                                                      n; 248 AA.
derived D
                                                      derived
                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                      Score
Pred.
                                                                                                                                                                                                                      Score 462.5; DB 8; Pred. No. 9.2e-28;
                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                        No.
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No.
                                                                                      462.5; DB 8;
No. 9.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                             464; DB 6;
No. 6.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466.5; DB 7
No. 4.7e-28;
                                                      SEQ
                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5; DB 5;
5.8e-28;
                                                                                                                                                                                                                                                                                                                                                       .5; DB 8
8.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.
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                                                                                                                                                                                       SEQ ID
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                                                                                                                                                                                                                                                                                                                        131
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                                                       #4
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                                                                                                                                                                                                                                   248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO:4
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Query Match
Best Local S
RESULT 1363
                                               Best Local Similarity RESULT 1369
                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1368
                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1367
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Best Local Similarity
RESULT 1362
                                                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Human KLK2.
WO200053776-A2.
14-SEP-2000.
                                                  1892//03...
07-JUL-1999.
(HOFF) ROCHE DIAGNOSTICS GMBH.
33.4%; Score 459; DB 2;
                                                                                                                                                                                                                                                                                                                                             Human prepro-Trp226-glandular kallikrein-2.
W09701630-Al.
                                                                                                                                                                                                                                                   AAU98921 standard; protein; 245 Human prostate specific antigen W0200240059-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP27546 standard;
Human kallikrein-3
                                                                                                             EP927764-A2.
                                                                                                                         AAY08894 standard; protein; 238 AA. Chimeric serine protease FXT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1995.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR84668 standard; protein;
Prepro-hK2 kallikrein.
                                   AAB21314 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9530758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EXON-) EXONHIT THERAPEUTICS ry Match 33.6%; t Local Similarity 41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FR2848569-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP27545 standard;
Human kallikrein-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FR2848569-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004076614-A2.
                                                                                                                                                                                     (AMBI-) AMERICAN FOUND (MINC/) MINCHEFF M S. (LOUK/) LOUKINOV D I. (ZOUB/) ZOUBAK S.
                                                                                                                                                                                                                                                                                                                                          16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EXON-) EXONHIT THERAPEUTICS ry Match 33.6%; Local Similarity 41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR66036 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PILA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HERM/) HERMANN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L/) DAHL E.
E/) ROSENTHAL A.
M/) HERMANN K.
                                                                                                                                                                                                                                                                                                                             ORION YHTYMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILARSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; (KLK-3) E
                                   protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 297 AA. (KLK-3) EHT103 p
                                                                                                                                                                                                                                                                                                  E OY.
33.5%;
40.2%;
                                                                                                                                                             33.4%;
41.4%;
                                                                                                                                                                                                                                                                                                                                                                                                      33.5%;
40.2%;
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40.2%;
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40.2%;
                                                                                                                                                                                                                             BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 281 AA.
EHT103 protien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SA.
Score 462; DB 8;
Pred. No. 1.2e-27;
                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                               Score 459.5; DB 5; Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 462.5; DB 8;
Pred. No. 9.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 462.5; DB 8; Pred. No. 9.3e-28;
                                                                                                                                                                                                                                                              AA.
(PSA) variant.
                                                                                                                                                                                                                             RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462; DB
No. 1.1e-
                                                                                                                                                                                                                                                                                                     460.5; DB 2;
No. 1.4e-27;
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No. 1.4e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variant
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                                                                                                                                                                                                                                                                                                                  261;
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Best Local Similarity
RESULT 1377
                                                                                             PA
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Best Local Similarity
RESULT 1374
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Best Local S
RESULT 1373
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Best Local Similarity
RESULT 1370
                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                      AAW45397 standard; protein; 26
Prostate-specific glandular ka
W09802748-A1.
22-JAN-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
23.4%; 23est Local Similarity 40.8%; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW49085 standard; protein; 2
Wild-type human Kallikrein 2
WO9821365-A2.
22-MAY-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                         Prostate cancer marker protein, 261
W02103009814-A2.
06-FRB-2000
                                                                                                             AAU06279 standard; protein; 261 AA.
Human Kallikrein2 polypeptide.
WO200145728-A2.
                                                                                       28-JUN-2001.
(EPIM-) EPIMMUNE INC.
                                                                                                                                                                                           WO200053776-A2.
                                                                                                                                                                                                            AAB21318 standard;
                                                                                                                                                                                                                                                                                                AAW96189 standard; protein;
Prepro human Kallikrein 2 (p
W0985973-A1.
                                                                                                                                                                                                                                                 (MAYO-) MAYO FOUNDATION.
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                                       (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW83203 standard; protein;
Prostate-specific glandular
W09846795-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW06971 standard; protein; Prostate-specific glandular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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  MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUNT SINAI HOSPITAL. h 33.4%; Similarity 40.8%;
                                                                                                                                                                                                            protein;
                                                                      33.4%;
                                                                                                                                                   33.4%;
                                                                                                                                                                       HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                              33.4%;
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40.8%;
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                                                                                                                                                                                                                                                                                                           1; 261 AA.
(preprohK2).
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kallikrein p
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2 (hK2).
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c kallikrein :
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Pred.
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kallikrein p
   Score
                                                                    Score 458.5;
Pred. No. 2e
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Pred.
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Pred.
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Pred.
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   458.5;
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No.
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No.
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No. 2e-27;
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No. 2e-
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No. 1.9
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2e
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                                                                   DB
-27;
                                                                                                                                                  DB
-27;
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.9e-27;
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-27;
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Length
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                                                                                                                                                         Length
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                                                                             261;
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Best Local Similarity
RESULT 1384
ID ADA50546 standard; p:
DE Human prostate specif
PN W02003031569-A2.
PD 17-APR-2003.
Best Local
RESULT 1386
                                                                                                 Best Local
RESULT 1385
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Best Local Similarity
RESULT 1382
                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1383
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Best Local Similarity
RESULT 1380
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RESULT 1378
                   Query Match
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                                                        Human mature prostate specific a US2003059864-A1
                                                                                                                                                        ADA50546 standard; protein; 237 Human prostate specific antigen W02003031569-A2.
                                                                                                                                                                                                                                                    AAB19818 standard; protein; 237 AA. Prostate specific antigen elevated WO200066718-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate-specific antigen EP1043394-A2.
11-OCT-2000.
                              (MIKO/) MIKOLAJCZYK (RITT/) RITTENHOUSE
                                                                                                                                                                                                                                                                                                                                                                AAB19819 standard; protein; 237 AA Prostate specific antigen specific w020067030-A1.
                                                                                                                                                                                                                                                                                                                               (HYBR-) HYBRITECH INC.
(BAYU) BAYLOR COLLEGE MEDICINE.
                                                                                                                                    (CENZ )
                                                                                                                                                                                                                              (HYBR-)
(BAYU )
                                                                                                                                                                                                                                                                                                                                                         09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                            (SERA-) SERATEC GES BIOTECHNOLOGIE MBH.

"Y Match

"L' Local Similarity 41.6%; Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate specific anti W09810292-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW96187 standard; protein;
Human prostate specific ant:
WO9859073-A1.
30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAYO-) MAYO FOUNDATION.
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW83213 standard;
Prostate-specific;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
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22-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1998.
(CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocal Similarity
        Similarity
                                                                                                                                                                                                  HYBRITECH INC.
BAYLOR COLLEGE MEDICINE.
h 33.3%; Score
Similarity 41.6%; Pred.
                                                                                                           Similarity
                                                                                                                                  CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; protein;
antigen pr
                               ВS
       33.3%;
                                                                                                           33.3%;
                                                                                                                                                                                                                                                                                                         33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.3%;
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41.6%;
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41.6%;
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antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen
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    Score
Pred.
                                                                                                          Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 2.1e-27;
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                                                                         antigen
                                                                                                                                                                 AA.
(PSA/KLK3),
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N-terminal
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protein.
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      457.5; DB 6
No. 2.1e-27;
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No. 2.1e-27;
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No. 2.1e-27;
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No. 2.1e-27;
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No.
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No. 2.1e-27;
                                                                                                                                                                                                                                                                      benign
                                                                                                                                                                                                                                                                                                                                                                          benign
                                                                         (PSA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment
                                                                                                                                                                   SEO
                                                                                                                                                                                                                                                                      prostatic hyperplasia
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                 237;
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Best Local Similarity RESULT 1392
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ID AA
DE Ka
PN WO
PD 07
PA (H
Query Match 33.1%; Score
Best Local Similarity 43.8%; Pred.
RESULT 1394

ID AAY72523 standard; protein; 232 AA.
BE Human prostase antigen #1.
PN W0200104143-A2.
PD 18-JAN-2001.
                                                                                     B R R I
                                                                                                                                RESULT
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Best Local (
                                                                                                                                                                                              AAW45400 standard;
Prostate-specific of WO9802748-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate specific antigen (PSA). US2003166036-A1.
                                                                                      Homo sapiens Tub Interactor WO9812302-A1.
                                                                                                                                                                                                                                                                                                 AAW06972 standard; protein; 261 AA Kallikrein prepro-hK2v217 variant. W09634964-A2.
                                                                                                                                                                                                                                                                                                                                                                                       ADJ59025 standard; protein; Human PSA mature protein sec
WO2003047506-A2.
                                                  (MILL-) MILLENNIUM PHARM INC.
ry Match 33.1%;
t Local Similarity 43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9802748-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW45398 standard; protein;
Prostate-specific antigen pı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOT-) BIOTECHN RES PARTN.
(CALB-) CALIF BIOTECHNOL INC.
ry Match 33.2%;
t Local Similarity 39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human kallikrein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP70677 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MIKO/) MIKOLAJCZYK S D.
(RITT/) RITTENHOUSE H G.
ry Match 33.3%;
t Local Similarity 41.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ59023 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAYO-) MAYO FOUNDATION.
HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.

ry Match
33.3%; Score 457.5; DB 7
Local Similarity
41.6%; Pred. No. 2.1e-27;
                                                                                                                                                               HYBR-) HYBRITECH
                                                                                                                                                                          MAYO-) MAYO FOUNDATION.
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                          l; protein;
glandular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 24
ene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                            33.2%;
41.6%;
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40.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   33.2%;
41.6%;
                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n; 237 AA.
protein h
                                                                                                         232 AA.
(hTI-1)
                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                           237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245
                                                                                                                                                                                                          261 AA.
kallikrein hK2v217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 AA
                                                   Score
Pred.
                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 456; DB 1;
Pred. No. 2.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                           Score 455.5; DB 2; Pred. No. 3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ያ
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C
                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                          455
No.
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                                                     454.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    455
No.
                                                                                                          protein
                                                                                                                                          5.5; DB 2;
3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PSA)
                                                     .5; DB 2;
3.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5; DB 8;
2.1e-27;
                                                                                                                                                                                                                                                                                                                                             .5; DB 7;
3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                .
5
                                                                                                                                                                                                                                                                                                                                                                                                                                     3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                Length
                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                         237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                237;
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Best Local
RESULT 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
RESULT 1399
                                                                                                                    Best Loca
RESULT 1402
                                                                                                                                                                                                                                          Best Local Similarity RESULT 1401
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
RESULT 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1397
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                            // ANY DOUDDATION.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
22.9%;
FY Match 32.9%;
The Local Similarity 41.8%;
                                                                          AAW96188 standard; protein; 244
Pro human Kallikrein 2 (prohK2).
WO9859073-Al.
                                                                                                                                                                                                            AAW45396 standard; protein;
Prostate-specific glandular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO38617 standard; protein;
Prostate Specific Antigen (I
US2004058881-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR84669 standard; protein; Pro-hK2 kallikrein. W09530758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU74930 standard; protein; 232 AA.
Amino acid sequence of prostase protein
WO200200867-A1.
                                                                                                                                                                                                    WO9802748-A1.
                                                                                                                                                                                                                                                                                                                       Prostate-specific WO9846795-A1.
                                                                                                                                                                                                                                                                                                                                                AAW83204 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PSA analogue
WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ59027 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ANTI-) ANTIGEN EXPRESS INC.
ry Match 33.1%;
t Local Similarity 39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
ry Match
13.1%; Score 454.5;
t Local Similarity 43.8%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. ry Match 33.1%; Score 454. t Local Similarity 43.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU74769 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS (CORI-) CORIXA CORD
                                                                                                                                                                                     22-JAN-1998
                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L6-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
            MAYO FOUNDATION.
YOUNG C Y F.
TINDALL D J.
KLEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYBRITECH INC
                                                                                                                                                                                                                                                                                                                                                                             DEPT HEALTH & HUMAN SERVICES
33.0%; Score 453.1
nilarity 41.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                    l; protein;
glandular
                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 237 AA. (Y154) mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.1%;
41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 232 AA.
prostase homologue
                                                                                                                                                                                                                                                       32.9%;
41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.1%;
43.8%;
32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PSA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             237
                                                                                                                                                                                                              244 AA.
kallikrein
                                                                                                                                                                                                                                                                                                                                     244 AA.
kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 AA
                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
Score 452.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 454.5; DB Pred. No. 4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 454.5; D
Pred. No. 3.5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 454.5; DB 4
Pred. No. 3.5e-27;
                                                                                                                                 452
No.
                                                                                                                                                                                                                                                       452
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454
No.
                                                                                                                                                                                                                                                       2.5; DB 2;
5.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5; DB 2;
3.7e-27;
                                                                                                                                                                                                                                                                                                                                                                              .5; DB 7;
4.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5e-27;
                                                                                                                                  .5; DB 2;
5.3e-27;
                                                                                                                                                                                                               precursor
                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
2
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                                                                                                                                                                                                                                                                                                                                     phK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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Length
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                                                                                                                                                                                                                                                                      244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232;
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Query
Best Loc.
RESULT 1409
ID AAW453°
DE Matur
PN WO9°
PD 22
PA /
PA /
                       Best Local Similarity
RESULT 1411
                                                                        PA PA
                                                                                                                                                         RESULT 1410
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
RESULT
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                                                Query Match
                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
ADA50561 standard; protein; 237 AA. Kallikrein KLK2, SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                             Prostate-specific glandular kallikrein WO9846795-Al.
                                                       (MAYO-) MAYO FOUNDATION
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                   AAW96186 standard; protein;
Mature human Kallikrein 2 (1
W09859073-A1.
                                                                                                                                                                                                                            AAW45395 standard; protein; 237 AA.
Mature prostate-specific glandular kallikrein hK2
W09802748-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAR77098 standard;
Prostate-specific
WO9528498-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKZON-OOJ
18-JUN-2004.
(EXON-) EXONHIT THERAPEUTICS SA.
21.9%; Score
32.9%; Score
41.8%; Pred.
                                                                                                        0-DEC-1998
                                                                                                                                                                                        (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-2003.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
xy Match 32.9%; Score 451.5; DB 7;
41.6%; Pred. No. 6.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PSA analogue
                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP27537 standard; protein; 297 AA.
Human kallikrein-2 (KLK-2) EHT102 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP27538 standard;
Human kallikrein-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW03130 standard;
Prostate-specific a
                                                                                                                                                                                                                                                                                                                                                                            (OYCO) UNIV COLUMBIA NEW YORK.

CY Match 32.8%; Score

Local Similarity 40.7%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ59029 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EXON-) EXONHIT THERAPEUTICS 
ry Match 32.9%; 
t Local Similarity 41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FR2848569-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9621042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L1-JUL-1996.
(UYBO-) UNIV BOSTON.
                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; protein; 237 AA. antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 236 AA. (L155/Y154) mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 281 AA. (KLK-2) EHT102 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                  32.8%;
42.0%;
                                                                                                                                                                 32.8%;
                                                                                                                                                                                                                                                                         32.8%;
42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.8%;
                                                                                                                                n; 237 AA.
(hK2).
                                 Score
Pred.
                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCORE Pred.
                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   æ
                                  450.5; DB 2
No. 7.4e-27;
                                                                                                                                                                450.5; DB 2;
No. 7.4e-27;
                                                                                                                                                                                                                                                                         450.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                               450.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452.5; DB 2;
No. 5.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452.5; DB 8;
No. 6.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                       7.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                 75.
                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                               ; DB 2;
.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           b variant
                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                            Length
                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SeqID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SeqID
                                            237;
                                                                                                                                                                            237;
                                                                                                                                                                                                                                                                                    237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236;
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Query Match
Best Local Similarity
RESULT 1412
ID AAR84667 standard; p
                                                                                               Query Match
Best Local Similarity
RESULT 1416
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
RESULT 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
RESULT 1413
           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                         AAW83212 standard;
hK2 variant A217V.
WO9846795-A1.
                 (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
                                                                                               (SMIT/)
                                                                                                              (MILL/)
(SCIO/)
(ELLE/)
                                                                                                                                              (RIEG/
                                                                                                                                                                                                                                                                                                                      ADJ83076 standard; protein; 217 / Trypsin protein which is related US2003170630-Al;
                                                                                                                                                                       (GANG/
                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide hom WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI17277 standard; protein; Polypeptide homologous to a WO200268649-A2. 06-SEP-2002.
                                                                                                      (MACD/
                                                                                                                                                                                                                                                                                                                                                                                                       ADI17269 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR84667 standard;
Mature kallikrein l
WO9530758-A1.
                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-1995.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003031569-A2.
17-APR-2003.
(CENZ) CENTOCOF
                                                                                                                                                                                       BOLD,
                                                                                                                                                                                                CASM/
                                                                                                                                                                                                                                                                                SPYT/)
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
                                                                                            ) MACDOUGALL (
                                                                                                                     PERNANDES E R.
RIEGER D K.
EDINGER S R.
GUNTHER E.
MILLET I.
SCIORE P.
                                                                                                                                                                     CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
  Similarity
                                                                                                                                                                                                           SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CENTOCOR INC.
                                                                                                             ELLERMAN K
                                                                                                                                                                                                                                                                                       LIU X.
                                                                                                                                                                                                                                                                                               ALSOBROOK J P. TCHERNEV V T.
                                                                                                                                                                                                                                                                                                                                                                                                homologous to a
                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
hK2.
                                                          protein;
32.6%;
                                                                           32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                        32.6%;
                                                                                                     ₽.
                                                                                                                                                                                                                                                                                                                                                       32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.8%;
42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.6%;
                                                           237
Score 447.5; DB 2;
Pred. No. 1.3e-26;
                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                       217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 AA.
human N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
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Pred.
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Pred. No. 7.
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No. 1.1e-26;
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.1e-26;
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1.4e-27;
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RESULT 1425
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Best Local
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(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                               AAR94526 standard; protein; Korean Viper Salmosa thromb
EP707067-A2.
                                                                                                                                                                                                                                                                                                                                        ABM82643 standard; protein; 227 A Human diagnostic and therapeutic WO2004023973-A2.
                                                                                         AAG79000 standard; protein; Mamushi fibrinolytic enzyme
                                                                                                                                                                                                                                                        AAR84670 standard; protein;
Mature kallikrein hK2.
WO9530758-A1.
 AAM52944 standard;
Agkistrodon halys |
                                                                                KR2001045716-A.
                                                                                                                                         (MOGA-) MOGAM BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR84671 standard; protein;
Mature kallikrein hK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TEXA ) UNIV TEXAS SYSTEM.
ry Match 32.4%;
t Local Similarity 41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW11023 standard; protein; 240 Human prostate specific antigen. W09640754-A1.
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Variant human Kallikrein 2
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                                                   (LEEJ/) LEE J W.
(PARK/) PARK W.
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                                                                                                                                                                                                                           HYBR-) HYBRITECH
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                                                                                                                                                                                                                                     MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                Local Similarity
                             local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
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µman Kallikrein 2 (hK2)
                                                                                                                                                                                                      I INC.
32.1%;
y 40.9%;
; protein; 260 AA.
brevicaudus thrombin-likle protease, salmobin.
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41.1%;
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42.0%;
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42.0%;
                              31.8%;
37.9%;
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thrombin-like
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(hK2).
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brevinase
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No. 2.
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No.
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No. 3.6e-26;
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No. 2.1e-26;
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No. 1.3e-26;
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No. 1.3e-26;
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Best Local Similarity
RESULT 1426
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RESULT 1434
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RESULT 1431
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RESULT 1430
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Best Local Similarity
RESULT 1427
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                                                                                                                                                                              AAM01120 standard; protein; 205 AA. Human prostate-specific amino acid W0200151633-A2.
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Pry Match 31.3%;
St Local Similarity 39.2%;
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30-MAR-1998.
(MOKA-) MOKAM BIOTECHNOLOGY RES INST.
21.7%; SCOTE 436;
31.7%; SCOTE 436;
31.1%; Pred. No. 1.
                                                                                                                                                                                                                                                                             Human prostate tumour US2002090372-A1.
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Human immunogenic F
WC200004149-A2.
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27-AUG-1998.
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                                                                                  Human prostate cDNA WO200173032-A2.
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(CORI-) CORIXA CORP.
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Human prostate cancer-related intracellular
 AAB74803 standard; protein;
Prostate tumour antigen prec
                                                                                                           AAU69766 standard;
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                                                                                                                                                                                                                                                                                                                ABG94414 standard;
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Pred. No. 4.5e-25;
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Pred. No. 4.5e-25;
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No. 4.5e-25;
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No. 4.5e-25;
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No. 4.5e-25;
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RESULT 1438
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Best Local Similarity
RESULT 1436
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RESULT 1435
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                                                                                                                                                           ABB95225 standard; protein;
Human P703P-DE13 protein SB
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                                                                                                                                                                                                                                  AAU04964 standard; protein;
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12-APR-2001.
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Prostate cancer specific ant
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FANGER G R.
RETTER M W.
STOLK J A.
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MITCHAM J L.
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VEDVICK T S.
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MITCHAM J L.

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amino acid
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SEQ ID NO 176
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Pred. No. 4.5e-25;
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No. 4.5e-25;
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No. 4.5e-25;
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No. 4.5e-25;
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Query Match
Best Local Similarity
RESULT 1446
ID AAB31579 standard; p
DE Amino acid sequence o
PN W0200078332-A2.
PD 28-DEC-2000.
                          B R B I
                                                                     Best Local Similarity RESULT 1447
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RESULT 1441
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                                                                                                                                                                                                          Human protein modification a WO2003031939-A2.
                                            ADE15982 standard; protein;
G-coupled protein receptor r
                                                                                                                                                                                                                                                                                                    Novel human polypeptide SeqID9039.
W0200216439-A2.
28-FER-2002
                                   G-coupled protein WO200283841-A2.
                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC

ry Match
t Local Similarity 37.8%;
                                                                                                                                                                                                                                                                                                                                                                                Deinagkistrodon acutus venom
CN1181421-A.
13-MAY-1998.
(SHAN-) SHANGHAI BIO-CHEM INS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG26042 standard; protein; 205 AA. Human prostate-specific polypeptide #6. US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR54337 standard; protein; 205 / Prostate tumour specific protein W0200289747-A2.
                (CURA-)
                                                                                                     (BJAR/) BJARNASON J
                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                   28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUB13626 standard; protein;
Human prostate specific prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate tumour protein
                                                                                                                                                                                                                                                                                                                                                                                                                           ABB09589 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB13626 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002081580-A1.
27-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG76668 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (XUJJ/) XU J.
(DILL/) DILLON D
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
              CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                       SHANGHAI BIO-CHEM INST CHINESE h 30.7%; Score 422. Similarity 36.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORIXA CORP.
                                                                                                                                      peptide;
e of cod t
                                                                             1 B.
30.6%;
44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
otein #6.
                                                                                                                                                                                                                                                               30.7%;
  30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.0%;
43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.0%;
43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.0%;
43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.0%;
43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.7%;
                                                                                                                                                                                 INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ein; 205
protein
                                             related
                                                                                                                                     ; 225 AA.
I trypsin
                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                              234 AA.
m thrombin-like
                                                                                                                                                                                                                                         218 AA.
                                                                                                                                                                       Score
Pred.
                                                                              Score
Pred.
                                                                                                                                                                                                                                                               Score
Pred.
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.5e-25;
                                                                                                                                                                                                                             maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
1 P703P-DE13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
 420;
                                                                             421; DB 4;
No. 1.3e-24;
                                                                                                                                                                        422; DB 6;
No. 1.1e-24;
                                             polypeptide,
                                                                                                                                      isozymes
                                                                                                                                                                                                                                                               422.5; DB 5;
No. 1.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 4.5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 426.5; DB 7;
No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426.5; DB 7
No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426.5; DB 6;
No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                       .5; DB
1e-24;
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 В
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                                                                                                                                                                                                                             molecule-4 (PMMM-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
e-25;
                                                                                                                                                                                                                                                                                                                                                                                                               protein
 7;
                                                                                                                                                                                                                                                                                                                                                                  SCI.
DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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Length
                                             SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                               (234
                                              ij
 218;
                                              No
                                                                                                                                                                                                                                                                                                                                                                                                               residue variant).
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LOGAL SIMILARITY

MATCH

MATCH
                                                                                                                                                                                                                                                                                                                                        Query
Best I
RESULT
ID AP
DE HI
PN W
PD 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1449
ID AAY28641 standard; p
DE Human secreted prote
PN W09940183-A1.
pD 12-AUG-1999
PA (HUMA) HUMAN GENOME
                                                                                                                                                                                                                                                                  Query
Best L
RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESU
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW46773 standard; protein; 233 AA.
Amino acid sequence of Salmonase.
EP814164-A2.
29-DEC-1997.
29-DEC-1997.
(MCGA-) MCGAM BIOTECHNOLOGY RES INST.
Query Match
30.4%; Score 417.
Puery Match
36.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-1999.

(HUMA-) HUMAN GENOME SCI INC.

30.4%;

31ry Match 30.4%;

46.1%;
                                                                                                                                                                                   Trypsin domain consensus US2002165152-A1. 07-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                 Human trypsin d
WO200226802-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY28641 standard; protein; Human secreted protein from WO9940183-A1.
                                                                                                                                                                                                                                               ABG75786 standard; protein; 226
                                                                                                                                                                                                                                                                                                                                                                                                            AAE21442 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL93921 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G-coupled
US2004006205-A1.
                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHEN)
                                                                                                                                                                 KAPE/) KAPELLER-LIBERMANN
                                                                                                                                                                                                                                                                    Local Similarity
1452
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATTURAJAN M.
BURGESS C E.
MALYANKAR U M.
SHIMKETS R A.
TAUPIER R J.
EDINGER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MILLER C E.
SPYTEK K A.
ZERHUSEN B E
PENA C E A.
SHENOY S G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MACDOUGALL J R.
RASTELLI L.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITHSON G.
CASMAN S J.
BOLDOG F L.
VOSS E Z.
VERNET C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZHONG M.
MEZES P S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GERLACH
LIU X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAZUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZHONG H.
SMITHSON
                                                                ndard; protein;
protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                      dard; protein; 226 AA.
domain consensus protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Þ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein receptor-related protein #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö.
                                                                                                                         30.3%;
42.6%;
                                                                                                                                                                                                                                                                                    30.3%;
42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.6%;
37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
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                                                                                                                                                                                                                           веquence,
                                                                                                                                                                 , D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AA.
cDNA clone
                                                                    198 AA
NO:96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                      Score
Pred.
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Pred.
                                                                                                                           Score 416.5; DB 6;
Pred. No. 2.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 , 417.5;
No. 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418;
No. 2
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No. 1.
                                                                                                                                                                                                                             SMART
                                                                                                                                                                                                                                                                                      416.5; DB 5;
No. 2.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 2;
.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 233;
                                                                                                                                                                                                                                                                                                       Length
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Query Match
Best Local S
RESULT 1454
                                                                                                                                                                                                                       Query Match
Best Local S
RESULT 1455
                                   Best Local Similarity
RESULT 1458
                                                                                               Query Match
Best Local Similarity
RESULT 1457
                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1456
                                                  Query Match
                                                                                                                                                                          Query Match
                                                                  Human diagnostic and therape w02004023973-A2.
                                                                                                                               Human protein modification a W02003083084-A2.
                                                                                                                                                                                        ADAS0560 standard; protein; 194 AA. prostate specific antigen (PSA/KLK3), WO2003031569-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV18c.
US2004038223-A1.
             Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN62900
                            ABM83248 standard;
                                                          (INCY-) INCYTE
                                                                 25-MAR-2004.
                                                                                                                      (INCY-) INCYTE CORP.
                                                                                                                                                                                 (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                          (SHIM/
(ROTH/
                                                                                                                                                                                                                                                                                                                                                                             (ANDE/
                                                                                                                                                                                                                                                                                                                                                                                                                   (YALY)
                                                                                                                                                                                                                                                                                                                                                                                                                                        (PATT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KEKU/)
                                                                                                                                                                                                                                                                                                                                                                                             ZERH
                                                                                                                                                                                                                                            GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                           AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                 MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M D.
LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                PATTURAJAN I
SPYTEK K A.
EDINGER S R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMITHSON G.
MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                             GORMAN L.
ZERHUSEN B
ANDERSON D
ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                            ELLERMAN K.
MALYANKAR U M.
ORT T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LI J.
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                      EISEN A.
INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                      CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                    d; protein; 299 AA.
and therapeutic pp
                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽.
                                                                                                                                                                                                                                                                                                                                                                                     ₹ ∪
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                               30.0%;
                                           29.8%;
37.1%;
                                                                                                       29.8%;
                                                                                                                                                                   29.8%;
38.7%;
                                                                                                                                                                                                                                                                                                           M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.0%;
                                                                                therapeutic
                                                                                                                                             and
                                                                                         215
                                                                                                                                                    215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
                                                                                                      Score
Pred.
                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                              Score
Pred.
                                            Score 409; DB 8;
Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 412.5; DB 6
Pred. No. 5.2e-24;
                                                                                                                                             maintenance molecule
                      pprotein
                                                                                pprotein
                                                                                                                                                                   409;
No. 9.
                                                                                                        409;
No. 1.
                                                                                                                                                                                                                               412.5; DB 8;
No. 5.2e-24;
                                                                                                                                                                                                        SEQ
                                                                                                        DB 7;
.1e-23;
                                                                                                                                                                    DB 6;
.5e-24;
                      SEQ
                                                                                 SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                         NO:15
                       ij
                                                                                 ij
                                                                                                            Length
                                                  Length 215;
                                                                                                                                                                          Length
                      NO:3497
                                                                                 NO:3078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 198;
                                                                                                                                                                                                                                       Length
                                                                                                                                            polypeptide
                                                                                                                                                                                                                                        198;
                                                                                                                                             SeqID8
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Query Match
Best Local Similarity
RESULT 1463
                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1462
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sest Local Similarity
RESULT 1459
                      A. contortrix protein; W09842850-A1.
                                                                                                                                                                                           AAB08510 standard; pro
A recombinant protein
WO200050612-A2.
                                                                                                                                                                                                                                                                                                                                                      ABM82641 standard; protein; 222 ABM82641 standard; protein; 22
  (RPMS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003029424-A2.
10-APR-2003.
(CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIT/) SMITHSON G.
(MILL/) MILLET I.
(PEYM/) PEYMAN J A.
(KEKU/) KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN62902 standard; protein; Human NOV18d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS2004038223-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) EISEN A.
) GANGOLLI E A.
) RIEGER D K.
) SPADERNA S K.
                                                                                                            INSTRUMENTATION LAB.:h 29.6%;
Similarity 36.2%;
RPMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A
ROTHENBERG M
LEACH M D.
                                                                                                                                                                                                                                                                                                               INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELLERMAN K.
MALYANKAR U
ORT T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDINGER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATTURAJAN M.
                                                                                                                                                                                                         protein; 230 AA.
ein C activator polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                       29.6%;
36.7%;
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                                               ein; 231 AA.
activator protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 6%;
                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                       Score
Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AA
NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 408.5; DB 6; Pred. No. 9.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 409;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                     pprotein
                                                                                                              406
No.
                                                                                                                                                                                                                                                                     407;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 408
No.
                                                                                                            1.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                               .5; DB 8;
9.6e-24;
                                                                                                                                                                                                                                                                     . 6e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                               fragment
                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                     8;
-23;
                                                                                                                                                                                                                                                                                        Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 299;
                                                                                                                                                                                                                                                                                                                                                                       NO:2890.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                181;
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Best Local Similarity
RESULT 1472
ID AAM52946 standard; p
DE Batroxobin, a snake
PN KR98002267-A.
PD 30-MAR-1998.
                                                                                                                                                     Query Match
Best Local Similarity
RESULT 1471
                                                                                                                                                                                                                                       Best Local Similarity RESULT 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
RESULT 1464
ID ABB09590
DE Deinagkis
                                                                                                                                                                                                                                                                                                                          Best Loca
RESULT 1469
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
RESULT 1465
                                                                                      Query Match
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                   Human trypsin de WO200226802-A2.
                                          AAM52946 standard; patroxobin, a snake
                                                                                                                                                                                                                                                                                         Batroxobin gen
JP02124092-A.
                                                                                                                                          AAE21441 standard;
                                                                                                                                                                                                       WO9929838-A1.
                                                                                                                                                                                                                    Araraca batroxobin
                                                                                                                                                                                                                             AAY17869 standard;
                                                                                                                                                                                                                                                                                                              AAR05436 standard;
                                                                                                                                                                                                                                                                                                                                                     01-MAR-1988.
(YAMA/) YAMASHINA I.
                                                                                                                                                                                                                                                                                                                                                                             JP63049084-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR20557 standard; protein; Fibrinogenolytic protein #4
                                                                                               (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                 (BRIM ) BRISTOL-MYERS
                                                                                                                                                                                                                                                                        (FUJI)
                                                                                                                                                                                                                                                                                                                                                                                                AAP81333 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibrinogenolytic DE4023699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM84665 standard;
Human diagnostic ar
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNITOTICE
13-MAY-1998
13-MAY-1998
(SHAN-) SHANGHAI BIO-CHEM INST CHINESE
29.5%; Score 405.
29.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INLI) INSTRUMENTATION LAB-
ry Match 29.4%;
t Local Similarity 37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200050612-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB08511 standard; protein;
Biosynthetic variant of prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deinagkistrodon CN1181421-A.
                                                                                                                                                                                                                                                                                  11-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB09590 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (BADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-2000
    Match
                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
             MOKAM
                                                                                                                                                                                                                                              FUJISAWA PHARM CO L'h 29.3%;
Similarity 32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                 candard; protein; gene product.
BIOTECHNOLOGY RES INST.
29.1%; Score 400;
                                                                                                                            uard; protein;
domain consens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acutus venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d; protein; 220 AA.
and therapeutic pprotein
                                          protein; 231 AA.
e venom protease.
                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                             RS SQUIBB
29.3%;
32.9%;
                                                                         29.2%;
                                                                                                                                                                                                                                                                                                                                  29.3%;
32.9%;
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36.7%;
                                                                                                                             consensus protein
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36.7%;
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36.2%;
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protein C a
                                                                                                                                                                                                                                                  Score
                                                                                                                                          249 AA
                                                                                                                                                                                                                             255
                                                                                                                                                                                                                                                                                                              255
                                                                          Score
Pred.
                                                                                                                                                             Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 AA.
                                                                                                                                                                                  8
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n thrombin-like
                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                 Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 1.
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No.
                                                                                                                                                             402;
No. 4
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No. 4
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No. 4
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                    403; DB 2;
No. 3.3e-23;
                                                                                                                                                             4.3e-23;
                                                                          .5; DB 5;
4.6e-23;
                                                                                                                                                                                                                                               ; DB 2;
4.3e-23;
                                                                                                                                                                                                                                                                                                                                 , DB 1;
4.3e-23;
                                                                                                                             #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5; DB
3e-23;
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5.5; DB 5;
2e-23;
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  BB
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. 2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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 Length
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                                                                                   Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:4914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                            255;
                                                                                                                                                                                                                                                                                                                                                                                                                              234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218;
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-A1.

// CAPELLER-L.

// KAPELLER-L.

// Match

Jest Local Similarity

RESULT 1479

ID ADE58223 stand*

DB Human Prote

PN W02003^*

PD 27-

PA
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ID AA
DE P1
PN JP
PD 06
PA (S
                                                                                                                                                                                                                                         RESULT 1478
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ID AB
DE Hu
PN WO
PD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dest Local Similarity
RESULT 1474
                                                                                                                                                                                                              BRBB
                                                                                                                          Query Match
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                  AAP70758 standard; protein; Pig pancreas elastase-2. JP62000276-A.
                                                                                                                                                                                                              ABG75785 standard; protein; 227 AA. Trypsin domain consensus sequence, US2002165152-A1.
                                                                                                                                                                                                                                                                                                                                               Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flaboxobin, a snake KR98002267-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse serine pr
W0200031243-A1.
                              AAE39992 standard; protein;
Human adipsin protein #1.
                                                                                                                                                                                                                                                                                          AAE39993 standard; protein;
Human adipsin protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM52945 standard;
                                                                                                                                                                ADE58223 standard; protein; 2
Human Protein P00746, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                ABM82831 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB11711 standard;
                                                                                                                                (GEHO ) GEN HOSPI
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOKA-) MOKAM BIOTECHNOLOGY
Y Match
Local Similarity 36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FUSO ) FUSO PHARM IND LTD
                                                                                                                                                                                                     KAPE/) KAPELLER-LIBERMANN
                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                         GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ndard; protein;
protease BSSP5
                                                                                                                                                                                                                                                                                                                                                       d; protein; 233 A and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                    LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
rotein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    venom
                                                   28.2%;
38.5%;
                                                                                                                                                                                      28.3%;
40.4%;
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39.1%;
                                                                                                                  28.3%;
38.5%;
                                                                                                                                                                                                                                                    28.5%;
38.0%;
                                                                                                                                                                                                                                                                                                                 28.5%;
36.8%;
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37.3%;
28
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. 28;
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1 protease.
                                                                                                                                                                                                     ₽.
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from sn
                                                                                                                                                                253 AA.
D NO 4094.
                                     253
                                                                                                    269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264
                                                                                                                                                                                                                                                                                                   253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RES INST
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                                                   Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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c pprotein
                                     ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                       snake venom.
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No. 3
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No. 1
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                                                                                                                  389;
No. 4
                                                                                                                                                                                                                                                     391;
No. :
387;
                                                     388;
                                                                                                                                                                                                                              PFAM
                                                                                                                                                                                                                                                                                                                  392; DB 8;
No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                               393; DB 2
No. 2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:4
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; DB 2;
1.7e-22;
                                                                                                                  ; DB 7;
4.3e-22;
                                                                                                                                                                                                                                                     ; DB 7
3e-22;
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                                                                                                                                                                                       w
                                                     DB 1;
.5e-22;
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.9e-22;
BB
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e-22;
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
253;
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Best Local Similarity
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Best Local Similarity
RESULT 1488
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                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1487
                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                        (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
                                                                                                                                          (DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                       ABM82644 standard; protein; 212 AA. Human diagnostic and therapeutic pprotein WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR39439 standard;
Human GENSET polype
WO2003014151-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB11710 standard; protein;
Human serine protease BSSP5
                                                                                                                                                                                                                                                                                       Tumour-associated WO2004030615-A2.
                                                                                         ADR66935 standard; protein;
Human prostatic carcinoma d
                                                                                                                                                                                                       ADR66037 standard; protein Human prostatic carcinoma WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus sequence WO2003031463-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2003
                                                                               WO2004076614-A2.
                                                                                                                                                                                                                                                                                                            ABM81778 standard;
                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM82830 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU09382 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FUSO ) FUSO PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200031243-A1.
                                                                                                                                                                         (HINZ/) HINZMANN B. (DAHL/) DAHL E.
                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2003
Similarity
                   PILARSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                    INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ıdard; protein; 264
polypeptide clone r
                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                d; protein; 212 AA.
and therapeutic pprotein
                                                                                                                                                                                                                                                                                                ; protein; antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ( IND LTD.
28.1%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 271 AA. of trypsin-like
                                                                                                                                                                                                                 protein; 213 AA
rcinoma derived ]
                                                                                                                                                                                                                                                                                                                                                                                                                28.1%;
36.3%;
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39.1%;
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36.8%;
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40.
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36.3%;
 40
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                                                                                                                       .0%;
. 24;
                                                                                         n; 213 AA.
                                                                                                                                                                                                                                                                                                264 AA.
target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 AA.
(hBSSP5)
                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 386; DB 6;
Pred. No. 7.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
Score 385;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   name
                                                                                          DNA
                                                                                                                       385;
No. 7.
                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386.5;
No. 7e-
                                                                                                                                                                                                                                                                                                                                385.
                                                                                                                                                                                                                                                                                                                                                                                                                385.
                                                                                                                                                                                                                                                385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
No.
                                                                                                                                                                                                                                                                                                  (TAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vCTRL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                          SEQ ID 233
                                                                                                                                                                                                                                                                                                                                                                                                                6.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5;
7e-
                                                                                                                                                                                                                                                 œ <u>i</u>5
                                                                                                                                                                                                                                                                                                                                .5; DB 8;
6.7e-22;
 DB 8;
.4e-22;
                                                                                                                                                                                                                                                ).4e-22;
                                                                                                                       . 4e
                                                                                                                                                                                                                                                                                                 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 271;
                                                                                          #4
                                                                                                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                   NO:2893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO:3079
                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 212;
                                                                                                                                                                                                                   #
                                                                                                                                                                                                                                                                                                  PRO2719,
                                                                                                                                                                                                                                                                                                                                          212;
                                                                                                                                                                                                                                                                                                  SEQ: 4580.
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Query Match
27.8%; Score 38
Best Local Similarity 37.2%; Pred. No
RESULT 1497
ID AAR05421 standard; protein; 250 AA.
DE Human adipsin/D encoded by a cDNA.
PN W09001540-A.
PD 22-FEB-1990.
PA (CALB-) CALIF BIOTECHN INC.
    Best Local Similarity
RESULT 1498
ID ADE58221 standard; F
DE Rat Protein AAB31922
PN WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1493
ID AAU79393 standard; p
DE Novel human kallikre
PN W02002014485-A2.
PD 21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1490
ID AAP6172
DE Porcine
PN JP61192
PD 26-AUG-
PA (KIRI)
                                                                                                                                                                                                            DE PN PA PA PA PA PA
                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA
PA
PA
PA
PA
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                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             08_APR-2004.
08_APR-2004.
(MOUN ) MOUNT SINAI HOSPITAL.
(MOUN ) MOUNT SINAI HOSPITAL.
27.8%;
ery Match
27.8%;
ADE59221 standard; protein; 263 AA.
Rat Protein AAB31922, SEQ ID NO 4092.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                              ABM82642 standard; protein; 212 A
Human diagnostic and therapeutic
WO2004023973-A2.
25-MAR-2004.
(INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUN-1990.
(BADI ) BASF AG.
(BACH/) BACH A.
                                                                                                                                                                      (BETH-) BETH ISRAEL HOSPITAL ASSOC.
(DANA-) DANA-FARBER CANCER INST.
(META-) METABOLIC BIOSYSTEMS INC.
(BETH-) BETH ISRAEL HOSPITAL ASSOC.

ry Match
27.8%; Score 382;
t Local Similarity 37.2%; Pred. No. 1.
                                                                                                                                                                                                                                                                             AAR05772 standard; protein; 250 AA. Human adipsin gene product from the clone W09006365-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN10933 standard; protein; 171 AA. Human kallikrein 15, marker of endocrine WO2004029285-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU79393 standard; protein; 171 AA. Novel human kallikrein KLK15, splice variant WO200214485-A2.
21-FEB-2002.
                                                         (CALB-) CALIF BIOTECHN INC.
ry Match 27.8%;
Local Similarity 38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR07513 standard; protein;
Ancrod-like polypeptide #2.
Ep395375-A.
                                                                                                                                                                                                                                                                    14-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 27.8%;
t Local Similarity 35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snake venom ancrod WO9006362-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR05775 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO INC. (KNOL ) KNOLL AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porcine elastase
JP61192289-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP61724 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KIRI ) KIRIN BREWERY KK.
ry Match 27.9%;
t Local Similarity 38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-1986.
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 272 AA. polypeptide.
                                                                                                                                                                                                                                                                                                                                    27.8%;
35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.9%;
                                                                                                                                                                                                                                                                                                                                                                                           , 212 AA.
Preutic pprotein s
                                                         Score 382;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 382.5; DB 8;
Pred. No. 9.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 383; DB 2;
Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                    382;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382.5; DB 5;
No. 9.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383; DB 2;
No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384; DB 1;
No. 1.1e-21;
                                                           DB 2;
.5e-21;
                                                                                                                                                                         DB 2;
.5e-21;
                                                                                                                                                                                                                                                                                                                                    DB 8;
.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer
                                                                                                                                                                                                                                                                                           phg31
                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #3
                                                                    Length
                                                                                                                                                                                      Length 250;
                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                            NO:2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171;
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Query Match
Best Local Similarity
RESULT 1499
ID ADN99596 standard; p
DE Novel human protein
                                                                                       Best Local Similarity RESULT 1500 ID ABU92049 standard;
   Best Local Similarity
                                                                                                                                Query Match
                                                                                                06-MAY-2004.

(EIVE-) FIVE PRIME THERAPBUTICS INC.

27.6%; Score 379.5; DB 8;

27.6%; Pred. No. 1.7e-21;
                                                    ABU92049 standard; protein; 220 AA.
Human protein modification and maintenance molecule-29
W02003031939-A2.
                                                                                                                                                                         ADN99596 standard; p
Novel human protein
WO2004038003-A2.
                                                                                                                                                                                                                                                            27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                              17-APR-2003.
INCYTE GENOMICS INC.
;h 27.6%;
Similarity 37.2%;
                                                                                                                                                                                     protein; 187 AA.
n sequence #412.
                                                                                                                                                                                                                               27.7%;
37.6%;
   Score
Pred.
                                                                                                                                                                                                                                 Score 381;
Pred. No. 1
 379;
No. 2.
                                                                                                                                                                                                                                 DB 7;
.9e-21;
   DB
2e
 -6;
-21;
             Length 220;
                                                                                                                                                                                                                                             Length
                                                                                                                              Length 187;
                                                                       (PMMM-29)
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